

Fri Oct 1 13:40:15 2004

us-09-869-582-12.rnpb

Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 82918, A  
Sequence 7, Appli  
Sequence 2810, Ap  
Sequence 10366, A  
Sequence 15806, A  
Sequence 44, Appl  
Sequence 14554, A  
Sequence 59, Appl  
Sequence 195, App  
Sequence 11512, A  
Sequence 43, Appl  
Sequence 31, Appl  
Sequence 718, App  
Sequence 718, App  
Sequence 3099, Ap  
Sequence 3103, Ap  
Sequence 14763, A  
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Sequence 3094, Ap  
Sequence 3104, Ap  
Sequence 3098, Ap  
Sequence 57, Appl  
Sequence 189, Appl  
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Sequence 1866, Ap  
Sequence 3101, Ap

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17 142.8 2.7 1062 9 US-09-978-382A-1  
18 142.8 2.7 1062 10 US-09-978-740A-1  
19 137.6 2.6 747 13 US-10-424-599-82918  
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24 123 2.3 5070 9 US-09-853-450-44  
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26 120.8 2.3 906 13 US-10-412-699B-59  
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45 111.4 2.1 265 12 US-09-922-293-3101

ALIGNMENTS

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; Sequence 21, Application US/09922293  
; Publication No. US2004012339A1  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Transcription in Plants  
; FILE REFERENCE: 16517.254  
; CURRENT APPLICATION NUMBER: US/09/922,293  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/067,000  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: US 60/069,472  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: US 60/071,479  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: US 60/074,201  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,282  
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; PRIOR FILING DATE: 1998-02-12  
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; PRIOR APPLICATION NUMBER: US 60/074,565  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/075,462  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/074,789  
; PRIOR FILING DATE: 1998-02-19

GenCore version 5.1.6  
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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	303.8	5.7	1054	10	US-09-849-772-3
3	303.8	5.7	1057	9	US-09-853-450-1
4	188.2	3.5	794	9	US-09-853-450-3
5	173.8	3.2	768	9	US-09-853-450-5
6	163.4	3.0	779	9	US-09-853-450-9
7	156.2	2.9	756	9	US-09-853-450-13
8	153	2.9	756	9	US-09-853-450-11
9	152.6	2.8	970	13	US-10-425-114-18693
10	151.8	2.8	1210	13	US-10-425-114-20049
11	151.8	2.8	1240	13	US-10-424-599-82915
12	150.2	2.8	697	17	US-10-767-795-5780
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; PRIOR FILING DATE: 1998-04-07
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; PRIOR FILING DATE: 1998-04-27
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; PRIOR FILING DATE: 1998-12-11
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; PRIOR FILING DATE: 1999-01-12
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; SEQ ID NO 21
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-922-293-21
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Qy 1713 GAAAACTTTCCTAAATGGTTCATACCAAGTCTGAGCTCTCTTATATCTCTCTGTA 1772
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Qy 1773 GTTTCCTATTTGGGGTCTTTGTTTGTGGTCTTTTAGAGTAAGAAGTTCTTAAAAA 1832
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Qy	2021	ATTCTTG	2027
Db	302	ATTCGTG	308
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; Publication No. US20020194645A1			
; GENERAL INFORMATION:			
; APPLICANT: Yanofsky, Martin F.			
; APPLICANT: Pelaz, Soraya			
; APPLICANT: Ditta, Gary			
; APPLICANT: The Regents of the University of California			
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants			
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development			
; FILE REFERENCE: 19452A-002400US			
; CURRENT APPLICATION NUMBER: US/09/853,450			
; CURRENT FILING DATE: 2001-05-09			
; NUMBER OF SEQ ID NOS: 61			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 1057			
; TYPE: DNA			
; ORGANISM: Arabidopsis thaliana			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (124)..(894)			
; OTHER INFORMATION: APETALA1 (AP1)			
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Qy	1721	TTCTTAATGGTTCATACCAAGCTCGAGCTCTCTTTATATCTCTCTCTGAGTCTTAA	1780
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Qy	1841	AAATGGGAAGGGGTAGGGTCAATTGAAGAGGTAGAGAACAGATCAATAGACAAGTGA	1900
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Qy	1901	CATTCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTG	1960
Db	182	CATTCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTG	241
Qy	1961	ATGCTGAAGTTGCTCTTGTGTGCTCTCCCATGAAGGGGAAACTTTCGAATACTCCACTG	2050
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Db	302	ATTCGTG	308
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; Publication No. US20020194645A1			
; GENERAL INFORMATION:			
; APPLICANT: Yanofsky, Martin F.			
; APPLICANT: Pelaz, Soraya			
; APPLICANT: Ditta, Gary			
; APPLICANT: The Regents of the University of California			
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants			
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development			
; FILE REFERENCE: 19452A-002400US			
; CURRENT APPLICATION NUMBER: US/09/853,450			

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; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
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; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Brassica oleracea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(794)
; OTHER INFORMATION: APETALA1 (AP1)
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Matches 207; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Db 1 TCTTAGAGGAAATAGTTCCTTTAAAGGGAT-AAAAATGGGAAGGGGTAGGTTCAAGTTG 59

QY 1867 AAGAGGATAGAGAACAGATCAATAGACAGTGCATTTCTCGAAGAGAGCTGGTCTT 1926
Db 60 AAGAGATAGAAACAGATCAATAGACAGTGCATTTCTCGAAGAGAGAGCTGGTCTT 119

QY 1927 TTGAAGAAAGCTCATGAGATCTCTGTTCTGTGATGCTGAAGTTGCTTGTGCTTC 1986
Db 120 ATGAAGAAAGCTCATGAGATCTCTGTTCTGTGATGCTGAAGTTGCTTGTGCTTC 179

QY 1987 TCCATAAGGGGAACTCTCGAATACCTCACTGATCTTGG 2027
Db 180 TCCATAAGGGGAACTCTTGAATACCTCACTGATCTTGG 220

RESULT 5
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; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
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; FEATURE:
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US-09-853-450-5

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Db 1 ATGGGAAGGGGTAGGGTTCAAGTTGAAGAGGATAGAGAACAGATCAATAGACAAGTGACA 60

QY 1903 TTCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTGTGAT 1962
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QY 1963 CTGAGAGTTGCTCTTGTGTCTTCTCCCAATAGGGGAACTCTTCGAATACCTCCACTGAT 2022

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Db 121 GCTGAGTTGGCTTGTGTGTTCTTCTCCATAAGGGGAACTCTTTGAATACCCCACTGAT 180
QY 2023 TCTTG 2027
Db 181 TCTTG 185

RESULT 6
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; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 779
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(777)
; OTHER INFORMATION: CAULIFLOWER (CAL)
; NAME/KEY: modified_base
; LOCATION: (778)..(779)
; OTHER INFORMATION: n = g, a, c or t
US-09-853-450-9

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Matches 173; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 1899 GACATTCGCAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTTG 1958
Db 66 GACATTCGCAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTTG 125

QY 1959 TGATGCTGAAGTTGCTCTGTTGTTCTTCTCCATAAGGGGAACTCTTCGAATACCTCCAC 2018
Db 126 TGATGCCGAGGTTTCCCTTATTTGTTCTTCTCCATAAGGGGAACTTTGTCGAGTACTCTC 185

QY 2019 TGATTTCTTG 2027
Db 186 TGAATCTTG 194

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US-09-853-450-13
; Sequence 13, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61

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; SEQ ID NO 20049  
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; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB170-041-G10\_FU1  
US-10-425-114-20049

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Best Local Similarity 71.0%; Pred. No. 1.2e-18; Indels 0; Gaps 0;  
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QY 1805 TCTTTTAGAGTAAGAGTTCTTAAAAAGGATCAAAATGGAAGGGGTAGGGTTCAAT 1864

Db 247 TTTTCTTGGTTGTAAGGAAACAAAGAAAGAACTAAGATGGGAAGAGGTAGGGTACAGC 306

QY 1865 TGAAGAGGATAGAGAACAAAGATCAATAGACAGTTCATTCGAAAAGAGCTGGTC 1924

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QY 1925 TTTTGAAGAAAGCTCATGATCTCTTCTCTGTGATGCTGAAGTTGCTCTTGTGCT 1984

Db 367 TGTCTCAAGAAAGCTCATGAAATCTGTACTCTGTGATGCTGAGGTAGCTTTCATTATCT 426

QY 1985 TCTCCATTAAGGGAACCTCTCGAATCTCCACTGATTTCTTG 2027

Db 427 TCTCTCAAGAAAGAGCTCTTTGAGTATGCTACTGATTCAATG 469

## RESULT 11

US-10-424-599-82915

; Sequence 82915, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 82915

; LENGTH: 1240

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_45890C.1

US-10-424-599-82915

Query Match

Best Local Similarity 2.8%; Score 151.8; DB 13; Length 1240;

Matches 201; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 1745 CTGAGCTCTCTTTATATCTCTCTGTAGTTCTTATTTGGGGTCTTTGTTTGGTTGGT 1804

Db 199 CTCACCTCTTAGGGTTATTTTGTCTCCCTTTTCTTGTGGGAATTGGGTTGGTTGGT 258

QY 1805 TCTTTTAGAGTAAGAGTTCTTAAAAAGGATCAAAATGGAAGGGGTAGGGTTCAAT 1864

Db 259 TTTTCTTGGTTGTAAGGAAACAAAGAAAGAACTAAGATGGGAAGAGGTAGGGTACAGC 318

QY 1865 TGAAGAGGATAGAGAACAAAGATCAATAGACAGTCAATTCGAAAAGAGAGCTGGTC 1924

Db 319 TGAAGAGGATAGAGAACAAAGATCAATCGCAGGTAATTTCTCCAAAGAGAGGTGGT 378

QY 1925 TTTTGAAGAAAGCTCATGAGATCTCTGTCTCTGTGATGCTGAAGTTGCTCTTGTGCT 1984

Db 379 TGCTCAGAAAGCTCATGAATATCTGTACTCTGTGATGCTGAGTAGCTTTGATTATCT 438

QY 1985 TCTCCCATTAAGGGAACCTCTTCGAATATCTCCACTGATTTCTTG 2027

Db 439 TCTCTCACAAGGAAAGCTCTTTGAGTATGCTACTGATTCAATG 481

## RESULT 12

US-10-767-795-5780

; Sequence 5780, Application US/10767795

; Publication No. US20040181830A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Cao, Yongwei

; APPLICANT: Zhou, Yihua

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53534)B

; CURRENT APPLICATION NUMBER: US/10/767,795

; CURRENT FILING DATE: 2004-01-30

; NUMBER OF SEQ ID NOS: 117596

; SEQ ID NO 5780

; LENGTH: 697

; TYPE: DNA

; ORGANISM: Gossypium hirsutum

; FEATURE:

; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C8942\_1

US-10-767-795-5780

Query Match

Best Local Similarity 2.8%; Score 150.2; DB 17; Length 697;

Matches 192; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1827 TAAAAAAGGATCAAAAATGGGAGGGGTAGGGTTCAATTGAAGGATAGAGCAAGAT 1886

Db 121 TATTTAAAAAAAATCATGGGAAGAGGTAGGGTTCAATTTAAAAAGGATTGAAAACAAGAT 180

QY 1887 CAATAGCAAGTCACATTTCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAT 1946

Db 181 CAACAGACAAGTTACTTTTTCAAAAGAGAGCTGGTTTATTTGAAAAAGCTCATGAT 240

QY 1947 CTCTGTTCTCTGTGATGCTGAAAGTTGCTCTTCTGTTCTCTCCCATAGGGGAACTCTT 2006

Db 241 CTCTGTTCTTGTGATGCTGAAAGTTGCTTTAATTTCTTTTCCCATAGGGGAACTCTT 300

QY 2007 CGAATACCTCACTGATTTCTTGTAACTTCAACTTAATTTCTTTTAAAAAAAT 2061

Db 301 TGAGTACTCCACTGATTTCTGTATGGAAGAGATCTTGAACGCTATGAAAGGTAT 355

## RESULT 13

US-10-424-599-33823

; Sequence 33823, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 33823

; LENGTH: 969

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_130546C.1

US-10-424-599-33823

	Query Match	2.7%	Score 145.8	DB 13	Length 969
	Best Local Similarity	75.9%	Pred. No. 1.5e-17		
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QY	1810	TAGAGTAAGAAGTTTCTTAA	AAAAAGGATCAAA	AAATGGGAAGGGGTAGGGGTTCAAT	TGAAG 1869
DB	161	TTTATTTTCTTAAAGCAAAA	AAAAAGACAGTAATATGGGAAGGGGTAGGGTTCAGCT	TGAAG 220	
QY	1870	AGGATGAGAACAGATCAAT	TAGACAAGTGACATTTCTCGAAAAAGAGAGCTGGTCTTTTG	1929	
DB	221	AGGATGAGAACAGATCAAT	TCGGCAGGTAACTTTCTCCAAAAGAGAGAGCTGGGTACTC	280	
QY	1930	AAGAAAGCTCATGAGATCT	CTGTTCTCTGATGCTCGAAGTTCGTCTTGTTGTTCTCTCC	1989	
DB	281	AAGAAAGCACAGAGATCT	CTGTGCTCTGAGCGGTAGGTCGCTTTGATTGTTCTCTCC	340	
QY	1990	CATAAGGGGAACTCTTCGA	ATACTCACTGATTCTTGGTAAGTTCACATAATCTT	2046	
DB	341	CACAAAGGAAGCTCTTTGA	ATATGACACCGATCTTGGTAAATTAATATATATCAT	397	

## RESULT 14

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US-09-978-730-1
; Sequence 1, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000920US
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-730-1

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## Query Match

	Query Match	2.7k;	Score 142.8;	DB 9;	Length 1062;
	Best Local Similarity	81.7k;	Pred. No. 6e-17;		
	Matches 165;	Conservative	0;	Mismatches 37;	Indels 0; Gaps 0;
QY	1826	TTAAATAAGGATCAAAAATCGGAGGGTAGGGTTCAATTGAACAGGATAGAGAACAGA	1885		
Db	84	TTTGAAGAGAGAGAGATATGGAHAGAGTAGGGTTTCAGCTGAACAGAGATAGAGAACAGA	143		
QY	1886	TCAATAGACAAGTGACATTCGCAAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGA	1945		
Db	144	TCAATAGGCAAGTTACTTTCTCAAAGAGAGAAGGTCGGTTTGCTCAAGAAAGCTCATGAGA	203		
QY	1946	TCCTCTGTTCTCTGTGATGCTGAAGTTCGCTCTTGTGTCTTCTCCCATAAAGGGGAAACTCT	2005		
Db	204	TCCTCTGTTCTCTGGGATGCTGAGGTGCTCTCATCTGCTTTCTCTTCCAAAGGCCAACTCT	263		
QY	2006	TCGAATACTCCACTGATTTCTTG	2027		
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RESULT 15

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US-09-978-729A-1
; Sequence 1, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978, 729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-729A-1

Query Match          2.7%; Score 142.8; DB 9; Length 1062;
Best Local Similarity 81.7%; Pred. No. 6e-17;
Matches 165; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy      1826  TTAATAAAGGATCAAAAATCGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGA 1885
Db      84    TTTGAAGAGAGAGAGATATCGGAAGAGGTAGGGTTGAGCTGAAGAGATAGAGACAGA 143

Qy      1886  TCAATAGACAAGTGACATTCGAGAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGA 1945
Db      144  TCAATAGGCAAGTTACTTCTTCAAGAGAGAAGGTCTGGTTTGCTCAAGAAAGCTCATGAGA 203

Qy      1946  TCTCTGTCTCTGTGAGTCTGAAGTTGCTCTTGTGTGCTTCTCCCATAGGGGAACTCT 2005
Db      204  TCTCTGTCTCTGCGATGCTGAGGTTGCTCTCATCGTCTTCTCTTCCAAAGGCAACTCT 263

Qy      2006  TCGAATACTCCACTGATCTTG 2027
Db      264  TCGAATATTCACCGACTCTTG 285

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 18:50:20 ; Search time 12353 Seconds  
(without alignments)  
12976.620 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 55026578

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1:	em_estba:*
2:	em_esthum:*
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4:	em_estm:*
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8:	em_htc:*
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10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
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27:	em_gss_vrl:*
28:	gb_gss1:*
29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	413.6	7.7	435	28	B97569	B97569 F15K10T6B I
2	405.8	7.6	426	28	BH240291	BH240291 AUNIA62TR
3	356.4	6.6	383	28	BH240405	BH240405 AUNIA34TR
4	325.4	6.1	638	9	AU236519	AU236519 AU236519

5	316	5.9	509	9	AA067443	AA067443 26288 Lam
6	189.6	3.5	676	28	BH994331	BH994331 oeg92a11
7	176.2	3.3	646	28	BZ503616	BZ503616 BONAV25TR
8	162.4	3.0	779	28	BZ065259	BZ065259 11f48b05
9	160.2	3.0	503	9	AI992862	AI992862 701493815
10	150.2	2.8	694	28	BZ004972	BZ004972 oei76b05
11	148.8	2.8	813	29	CC946428	CC946428 BOIFJ10TF
12	148	2.8	811	28	BZ484352	BZ484352 BON0Z14TR
13	147	2.7	476	14	T42418	T42418 5681 Lambda
14	145.2	2.7	658	12	BG456966	BG456966 NF08D03P
15	145.2	2.7	665	12	BI263356	BI263356 NF089C12P
16	145.2	2.7	830	28	BH249426	BH249426 BOGAK13TR
17	143.8	2.7	440	9	AI100509	AI100509 34884 Lam
18	142.8	2.7	543	14	CB258385	CB258385 30-E01180
19	142.8	2.7	559	14	CB258393	CB258393 30-E01179
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21	139.6	2.6	200	29	BX288612	BX288612 Arabidops
22	138.6	2.6	353	14	CF510214	CF510214 USDA-FP 1
23	138.6	2.6	414	14	CF508545	CF508545 USDA-FP 1
24	138.6	2.6	626	14	CF507975	CF507975 USDA-FP 1
25	137	2.6	850	10	AW738740	AW738740 EST340167
26	136.6	2.5	734	13	B0872670	B0872670 Q045E11 P
27	135.6	2.5	680	13	BQ148488	BQ148488 NF068H07F
28	135.4	2.5	615	13	B0868189	B0868189 M112C09 P
29	134.4	2.5	550	13	B0995541	B0995541 QG10E16
30	134.4	2.5	594	13	B0997005	B0997005 QG14H02
31	134	2.5	680	28	BH953535	BH953535 odi84c02
32	132.6	2.5	755	9	AJ568205	AJ568205 AJ568205
33	130.8	2.4	467	10	AW266670	AW266670 LO-1492T3
34	130.8	2.4	707	10	BF479063	BF479063 L48-2708T
35	130	2.4	634	14	CA917484	CA917484 EST641631
36	129.8	2.4	777	10	BE034098	BE034098 MG05B05 M
37	129.2	2.4	694	10	BF479099	BF479099 L48-2745T
38	128.4	2.4	755	13	BQ988395	BQ988395 QGF14M24
39	128.2	2.4	613	12	BM406322	BM406322 EST580649
40	127.2	2.4	331	14	CA525666	CA525666 KS1205980
41	125.4	2.3	951	12	BG838400	BG838400 GC01_02C0
42	125.2	2.3	505	14	CF508148	CF508148 USDA-FP 1
43	124.6	2.3	459	14	CB086682	CB086682 h188F05G
44	124.4	2.3	537	14	CB610731	CB610731 ALBEDO000
45	123.4	2.3	304	14	CA523033	CA523033 KS12016H0

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RESULT 1	B97569	F15K10T6B IGF Arabidopsis thaliana genomic clone F15K10, genomic survey sequence.
LOCUS	B97569	435 bp DNA linear GSS 31-MAR-1998
DEFINITION	B97569	Survey sequence.
ACCESSION	B97569	GI:2999648
VERSION	B97569	GSS.
KEYWORDS	B97569	Arabidopsis thaliana (thale cress)
SOURCE	B97569	Arabidopsis thaliana
ORGANISM	B97569	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE	B97569	1 (bases 1 to 435)
AUTHORS	B97569	Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Adams, M.D. and Venter, J.C.
TITLE	B97569	A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3
JOURNAL	B97569	Unpublished (1997)
COMMENT	B97569	Contact: Steve Rounsley Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: rounsley@tigr.org

Contact: Chris Town

Feldblyum, T. V. and Fraser, C. M.

37

TITLE Survey sequencing of Arabidopsis thaliana BAC T17J15  
JOURNAL Unpublished (2001)  
COMMENT Other GSSs: AUTNA34TF  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
From Wash. U contig 1128.  
Seq primer: TR  
Class: sheared ends.

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[illegible]

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ORGANISM	Arabidopsis thaliana
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	Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
	Spermatophyta; Magnoliophyta; euangiosperms; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
REFERENCE	1 (bases 1 to 638)
AUTHORS	Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satoh, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Isai, Y.,

Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rtc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998) cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FIC-1 vector (Garninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

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	/lab_host="DH10B"
	/clone_lib="RAFLJ5"
	/note="Site 1: BamHI; Site 2: SalI"

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Qy	1761	ATCTCTCTTGAGTTCTTAATTCGGGGCTCTTTGTTTGTGTTCTTTTAGAGTAAGAA	1820		
Db	61	ATCTCTCTTGAGTTCTTAATTCGGGGCTCTTTGTTTGTGTTCTTTTAGAGTAAGAA	120		
Qy	1821	GTTCCTTTAAAAAGGATCAAAAATGGGAAGGGGTAGGGTTCAAATTGAAGAGGATAGAA	1880		
Db	121	GTTCCTTTAAAAAGGATCAAAAATGGGAAGGGGTAGGGTTCAAATTGAAGAGGATAGAA	180		
Qy	1881	CAAGATCAATAGACAAGTGACATTCTCGAAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCA	1940		
Db	181	CAAGATCAATAGACAAGTGACATTCTCGAAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCA	240		
Qy	1941	TGAGATCTCTGTTCTCTGTGATGCTGAAGTTGCTCTTGTGTTCTTCTCCCAATAAGGGAA	2000		
Db	241	TGAGATCTCTGTTCTCTGTGATGCTGAAGTTGCTCTTGTGTTCTTCTCCCAATAAGGGAA	300		
Qy	2001	ACTCTTCGAATACCTCCACTGATCTTG 2027			
Db	301	ACTCTTCGAATACCTCCACTGATCTTG 327			

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LOCUS	
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ACCESSION	AA067443
VERSION	AA067443.1 GI:1565776
KEYWORDS	EST.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi. 1 (bases 1 to 509)







ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 503)

REFERENCE  
AUTHORS Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,  
Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,  
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D.,  
Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C.,  
Carpio, T., Policky, J., Suzuki, G., Argentin, C., Shah, S.,  
Nobrega, A., Murre, L., Turner, C., Krikorian, S., Elder, L. and  
Hanson, D.

TITLE Arabidopsis thaliana Gene Expression MicroArray  
JOURNAL Unpublished (1999)  
COMMENT Contact: David Smoller, Ph.D.  
Genome Systems, Inc., a wholly owned subsidiary of Incyte  
Pharmaceuticals, Inc.  
4633 World Parkway Circle, St. Louis, MO 63134, USA  
Tel: 877-577-2733  
Fax: 314-427-3324  
Email: service@genomesystems.com.

FEATURES  
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/clone="701493815"  
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Best Local Similarity 63.0%; Pred. No. 3.6e-11;  
Matches 244; Conservative 0; Mismatches 136; Indels 7; Gaps 3;

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DB 1 AAGAAAACCTTCCTAATGGTTCATACCAAGCTGAGCTCTCTTATATCTCTTG 60

QY 1771 TAGTTCTTATGGGGCTTTGTTTCTTGTGTTCTTTTGTAGTAAGAAGTTCTTAAA 1830  
DB 61 TAGTTCTTATGGGGCTTTGTTTCTTGTGTTCTTTTGTAGTAAGAAGTTCTTAAA 120

QY 1831 AAGAGTCAAAATGGGAAGGGTGGGTCAATTGAAGAGATAGAGAACAAATCAAT 1890  
DB 121 AAGAGTCAAAATGGGAAGGGTGGGTCAATTGAAGAGATAGAGAACAAATCAAT 177

QY 1891 AGACAAGTGACATCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCT 1950  
DB 178 TGGCAAGTGACATCTTCGCAAGAGAA--TGGTCTTTTGTAGGAA--TCCTTAAACTCT 233

QY 1951 GTTCTCTGTGATGCTGAAGTTGCTTGTGTTCTCTCCATAGGGGAAGCTCTCGAA 2010  
DB 234 TTTTCTTAGGGGAAAATGACCTTTTGGGGCTCCCCCAAGGGGAAACCTCGGGGA 293

QY 2011 TACTCCACTGATCTTGTGTAACCTCACTAATCTTTTACTTTTAAAAAACTTTTAAATC 2070  
DB 294 AA 353

QY 2071 TGCTACTTTATAGTTTTCCTCC 2097  
DB 354 CGCGGAGAAAAAAGTTTTCCTCC 380

RESULT 10  
LOCUS BZ004972  
DEFINITION oel76b05.g1 B.oleracea002 Brassica oleracea genomic, genomic survey  
sequence.  
ACCESSION BZ004972  
VERSION BZ004972.1 GI:23553230  
KEYWORDS GSS.

ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 694)

REFERENCE  
AUTHORS Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,  
Nash, W., Rabinowicz, P.D. and Wilson, R.K.  
TITLE Whole genome shotgun reads from Brassica oleracea  
JOURNAL Unpublished (2002)  
COMMENT Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@watson.wustl.edu  
Place: oel76 row: b column: 05  
Seq primer: -28RPOT reverse  
Class: shotgun  
High quality sequence start: 38  
High quality sequence stop: 551.  
Location/Qualifiers  
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/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3712"  
/clone\_lib="B.oleracea002"  
/note="Vector: pOTw13; Whole genome shotgun library from  
flowering buds. DNA was purified from a crude nuclear  
prep using Brassica oleracea T0100DH3 buds provided by  
Thomas Osborn at the University of Wisconsin. Genomic  
DNA was provided by Pablo Rabinowicz (CSHL) and the  
shotgun library prepared at Washington University Genome  
Sequencing Center."

ORIGIN  
Query Match 2.8%; Score 150.2; DB 28; Length 694;  
Best Local Similarity 74.9%; Pred. No. 5.4e-10;  
Matches 188; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1826 TTAAAAAGGATCAAAATGGGAAGGGTGGGTCAATTGAAGAGGATAGAGAACAGA 1885  
DB 181 TTTGAAGAGAAGAGAGATGGGAAGGGGTAGGTTCACTGAAGAGGATAGAGATAAGA 240

QY 1886 TCAATAGACAAGTGACATCTCGAAAAGAGAGCTGTTCTTTGAAGAAAGCTCATGAGA 1945  
DB 241 TCAATAGACAAGTACTTTCTCAAGAGAAGCTCTGGTTGCTCAAGAAAGCTCATGAGA 300

QY 1946 TCTCTGTTCTCTGTGATGCTGAAGTGTCTTTGTTGTTCTTCTCCCATAGGGGAACTCT 2005  
DB 301 TCTCTGTTCTCTGGATGCTGAGGTGCTCTCATGCTCTTCTTCCAAAGGCGAACTCT 360

QY 2006 TCGAATATCCACATGATCTTGGTAACCTCAACTAATCTTTTACTTTTAAAAAATCTTT 2065  
DB 361 TCGAATATCCACAGACTCTTGGTAATATTATATATTTTATTTAACTCATAACTATATA 420

QY 2066 TAATCTGCTAC 2076  
DB 421 TTATAAGTTAC 431

RESULT 11  
LOCUS CC946428  
DEFINITION BOIFJ10TF BO.1.4.1.6\_KB\_nuc Brassica oleracea genomic clone  
BOIFJ10, genomic survey sequence.  
ACCESSION CC946428  
VERSION CC946428.1 GI:33779294  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 813)

**AUTHORS** Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
**TITLE** Whole genome shotgun sequencing of Brassica oleracea  
**JOURNAL** Unpublished (2001)  
**COMMENT** Other GSSs: BO10FJ10TR  
 Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF  
 Class: sheared ends.

**FEATURES**

source  
 1. .813  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BO10FJ10"  
 /clone\_lib="BO 1.4 1.6 KB nuc"  
 /notes="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared  
 nuclear DNA inserted into PHOS2 using BstXI linkers"

**ORIGIN**

Query Match 2.8%; Score 148.8; DB 29; Length 813;  
 Best Local Similarity 80.6%; Pred. No. 7.3e-10;  
 Matches 174; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 QY 1818 GAAGTTCTTAAAGGATCAAGATGGAAGGGGTGAGGTTCAATTGAAGAGGATAGA 1877  
 DB 7 GAGCTTTTGGGGGATACAGAGATGGGAAGGGGTAGGTTGAGTGGAGAGGATAGA 66  
 QY 1878 GAACAAGATCAATAGACAAGTGCATCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGC 1937  
 DB 67 AAACAAGATCAATAGCAAGTACTTCTCAAAAGAGAGCTGGTCTTGAAGAGC 126  
 QY 1938 TCATGAGATCTGTTCTCTGTGATGCTGAAGTTGCTCTTTGTTGCTTCCCATGAGG 1997  
 DB 127 TCATGAGATCTGTTCTCTGTGATGCTGAAGTTGCTCTTTGTTGCTTCCCATGAGG 186  
 QY 1998 GAACTCTTCGATCTCCACTGATCTTCTGTTACT 2033  
 DB 187 CAAACTCTTCAATATTCACCGACTCTTGGTAAT 222

**RESULT 12**

BZ484352 811 bp DNA linear GSS 13-DEC-2002  
 LOCUS BONO214TR BO 1.62 KB tot Brassica oleracea genomic clone BONO214,  
 DEFINITION genomic survey sequence.

**ACCESSION**

VERSION BZ484352

**KEYWORDS**

SOURCE GSS: BZ484352.1 GI:26786750

**ORGANISM**

Brassica oleracea  
 Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

**REFERENCE**

1 (bases 1 to 811)  
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
**AUTHORS** Whole genome shotgun sequencing of Brassica oleracea  
**TITLE** Unpublished (2001)  
**JOURNAL** Other GSSs: BONO214TF  
**COMMENT** Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.

**FEATURES**

source  
 1. .811  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BONO214"  
 /clone\_lib="BO 1.6 2 KB tot"  
 /note="Vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared  
 total DNA inserted into PHOS1 using BstXI linkers"

**ORIGIN**

Query Match 2.8%; Score 148; DB 28; Length 811;  
 Best Local Similarity 59.2%; Pred. No. 9.2e-10;  
 Matches 457; Conservative 0; Mismatches 215; Indels 100; Gaps 8;  
 QY 4189 ATGCTTTCTAAACAGGTAACATGTCATCATTTCTCTTTC-ATCAACATGTTGTCATT 4247  
 DB 1 ATGCTTTCTAAACAGGTAACATGTCATCATTTCTCTTTC-ATCAACATGTTGTCATT 60  
 QY 4248 GCATTAATCTTACCTTCCACTGTTCTGCTCCACATTCAGCCCAAGCTATACCT----- 4301  
 DB 61 ACATTAATTAATGCTTCTACTGTTTACTCCACATTCAGGCCAAGCTATTCCTACGACA 120  
 QY 4302 ACGATATCTCATATCTCCACTTAACCTCGGCACCATTAATAAATAAGAAAATCTTTG 4361  
 DB 121 ACGAATCTTCAATTTCTACATTTAGTTCACACCAATTCATAGAAAATAGTTGTTTAC 180  
 QY 4362 CAAATTTGTT-----TGAATAGCATAGATGTTGTTCTATTGATTGA 4402  
 DB 181 ATAGTCTATTGATTGATATCATCATCAGCGCGCTGTACATAGATGGCTTTGCCCATTTA 240  
 QY 4403 TATAATCACCAGCTGTAGTAGATGTTTGTCCGTTAGTTTAAAGTGTTCTCTCGG 4462  
 DB 241 GTTTTAAAGTTGTTCTTCAGATTGAAAACCTTCGTACCTCTCATCTTATTCTACTGCTCA 300  
 QY 4463 ATTGAAAATATTGTAATCTTTTGAATGTTTGTGCCATCTTCTTACTTAGTCTCATAT 4522  
 DB 301 TCTATATAGGTTATGAGAAATAGCCAGTACTAATTAATAAATAATTAAGTCCCAAT 360  
 QY 4523 CTATG-----TATATGAATATAGACACTCTCTCTAAATTATAAATGTTATAATA 4571  
 DB 361 TTTTGGAGCAGTTAAATAATAGTTTTCAGTAGATATATATTAAATAATGCAATAATAGTA 420  
 QY 4572 GTTCATTCGATGAGTGCACACTGTGAA-----AATTAATCTATTGTAACCA 4615  
 DB 421 GTTTATTGATGAGTGCAGGAACTAGGTGTAAACCAAGATCAAAATGTAGTTACATCTG 480  
 QY 4616 TTGCATATATATAGTT-----TCTTCACCTTTGAAAATTTGATGATGA----- 4656  
 DB 481 ATGCACATATCTATTGATTATGAAGTGTGCTCGCTCTGAAAATTTGATGATGATGATGAT 540  
 QY 4657 -TAATATGTTTGAATAATAATTTG-----CTGGCAGAT 4688  
 DB 541 GTAATATGCGATGGAACAAGTTGTTGTAACAAATTTGTTTAAACTGAGACTTGTTCAGAT 600  
 QY 4689 CAAGGAGAGGAAAAAATTTCTTAGGCTCAACAGGAGCAGTGGATGAGCAGACCAAGG 4748  
 DB 601 CAAGGAGAGGAAAAAAGGTTCTTATGGCACAACAAGAGCAATGGGACCAGAGAACCATGG 660  
 QY 4749 CCACAATATGCTCCCTCTGCGCAGCAGCAGCACAATCCAGCATCTTACATGCT 4808  
 DB 661 CCAAAATATGCTTTCGCCCGCCCGCCCGCAGCAGCACAATCCAGCATCTTACATGCT 720  
 QY 4809 CTCTCATGACCATCTCTTTTCTCAACATGGGGTAAACAAAAAATTACTAAT 4860  
 DB 721 CTCTCATGACCATCTCTTTTCTCAACATGGGGTAAACAAAAAATTACTAAT 772

**RESULT 13**

T42418  
 LOCUS T42418 476 bp mRNA linear EST 07-JAN-1998  
 DEFINITION 5681 Lambda-PRU2 Arabidopsis thaliana cDNA clone 113F9T7, mRNA

sequence.  
 T42418  
 VERSION T42418.1 GI:933190  
 EST  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE  
 AUTHORS Newman,T.; debruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M., Retzel,E. and Somerville,C.  
 TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 JOURNAL Plant Physiol. 106, 1241-1255 (1994)  
 MEDLINE 95148729  
 PUBMED 7846151

COMMENT  
 On Nov 29, 1993 this sequence version replaced gi:635006.  
 Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313tcn@bm.cl.msu.edu  
 Seq primer: 17.

## FEATURES

Location/Qualifiers  
 1..476

/organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /strain="var columbia"  
 /db\_xref="taxon:3702"  
 /clone="113P97"  
 /clone\_lib="Lambda-PRL2"  
 /note="Vector: Lambda Zip-Lox; Site 1: Sal; Site 2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."

## ORIGIN

Query Match 2.7%; Score 147; DB 14; Length 476;  
 Best Local Similarity 98.7%; Pred. No. 1.8e-09;  
 Matches 147; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1879 AACAGATCAATAGACAGTGCATTCGAAAGAGAGAGCTGCTTTTGAAGAAAGCT 1938  
 DB 1 AACAGATCAATAGACAGTGCATTCGAAAGAGAGAGCTGCTTTTGAAGAAAGCT 60

QY 1939 CATGAGATCTCTGTTCTGTGATGCTGAAGTTGCTTGTGTTGCTTCTCCCAAGGGG 1998  
 DB 61 CATGAGATCTCTGTTCTGTGATGCTGAAGTTGCTTGTGTTGCTTCTCCCAAGGGG 120

QY 1999 AAATCTTCGAAATCACTCCACTGATCTTG 2027  
 DB 121 AAATCTTCGAAATCACTCCACTGATCTTG 149

## RESULT 14

BG456966  
 LOCUS BG456966 658 bp mRNA linear EST 19-MAR-2001  
 DEFINITION NF098009PL1F1076 Phosphate starved leaf Medicago truncatula cDNA  
 accession BG456966  
 version BG456966.1 GI:13380291  
 keywords EST.

## SOURCE

ORGANISM Medicago truncatula (barrel medic)

Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

## REFERENCE

1 (bases 1 to 658)

## AUTHORS

Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.

## TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

## JOURNAL

Medicago truncatula phosphate-starved leaf library

## COMMENT

Unpublished (2000)

Contact: Harrison MJ

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7325

Fax: 580 221 7380

Email: mjharrison@noble.org

Insert Length: 658 Std Error: 0.00

Plate: 098 row: D column: 09

Seq primer: TCACACAGAAACACGTATGAC.

## FEATURES

Location/Qualifiers

1..658

/organism="Medicago truncatula"

/mol\_type="mRNA"

/db\_xref="taxon:3880"

/clone="NF098009PL"

/tissue\_type="leaf"

/dev\_stage="trifoliolate"

/clone\_lib="Phosphate starved leaf"

/note="Vector: Lambda Zap; At the trifoliolate stage, M.

truncatula plants were transplanted to phosphate-free sand

and grown for a further 30 days. During this 30 day

period, the plants were fertilized twice weekly with 1/2

Hoaglands solution containing only 20uM potassium

phosphate. RNA was prepared from above ground tissues."

## ORIGIN

Query Match 2.7%; Score 145.2; DB 12; Length 658;  
 Best Local Similarity 72.1%; Pred. No. 2.4e-09;  
 Matches 189; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1822 TTCTTAAAAAGATCAAAAATGGGAAGGGTAGGGTTCAATTCAAGAGGATAGAGAC 1881  
 DB 158 TTTCATTTCCAAACCAAAAATAATGGGAGGGAGAGTCAGTTGAAGAGATTGAGAAC 217

QY 1882 AAGATCAATAGACAAGTGCATTCGAAAAAGAGAGCTGCTTTTGAAGAAAGCTCAT 1941  
 DB 218 AAGATCAATAGACAAGTGCATTCGAAAAAGAGAGCTGCTTTTGAAGAAAGCACAA 277

QY 1942 GAGATCTCTGTTCTGTGATGCTGAAGTTGCTCTTGTGTTCTCTCCCAAGGGGAAA 2001  
 DB 278 GAGATCTCTGTTCTGTGATGCTGAAGTTGCTCTCTCTCTCTCTCTCTCTCTCTCT 337

QY 2002 CTCTTCCGAATCTCCACTGATTCCTTGGTAACCTCACTTAATCTTCTTCTTCTTCTTCT 2061  
 DB 338 CTCTTCTGAATCTCCAGGATCCTTGGTACGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 397

QY 2062 CTCTTCTGAATCTCCACTGATTCAT 2083  
 DB 398 TTATTATTATTATTATTATTAT 419

## RESULT 15

BI263356  
 LOCUS BI263356 665 bp mRNA linear EST 18-JUL-2001  
 DEFINITION NF089C12PL1F1098 Phosphate starved leaf Medicago truncatula cDNA  
 clone NF089C12PL 5', mRNA sequence.  
 accession BI263356  
 version BI263356.1 GI:14864514  
 keywords EST.  
 SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 665)  
REFERENCE Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
AUTHORS Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.  
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula phosphate-starved leaf library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Harrison, M.J.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7325  
Fax: 580 221 7380  
Email: mjharrison@noble.org  
Insert Length: 665 Std Error: 0.00  
Plate: 089 row: C column: 12  
Seq primer: TCACACAGAAACAGCTATGAC.  
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/clone="NF089C12PL"  
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/clone\_lib="Phosphate starved leaf"  
/note="Vector: Lambda Zap; At the trifoliolate stage, M.  
truncatula plants were transplanted to phosphate-free sand  
and grown for a further 30 days. During this 30 day  
period, the plants were fertilized twice weekly with 1/2  
Hoaglands solution containing only 20uM potassium  
phosphate. RNA was prepared from above ground tissues."

ORIGIN  
Query Match 2.7%; Score 145.2; DB 12; Length 665;  
Best Local Similarity 72.1%; Pred. No. 2.4e-09;  
Matches 189; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
Qy 1822 TTCTTAAAAAGGATCAAAAATGGGAAGGGTAGGGTTCAATTGAAGAGGATAGAGAAC 1881  
Db |||||  
202 TTTCATTTCCACCAAAAAATAATGGGAGGGGAAGAGTGCAGTTGAAGAGGATTGAGAAC 261  
Qy 1882 AAGATCAATAGACAAGTGACATTCTGAAAGAGAGAGCTGGTCTTTTGAAGAAAGCTCAT 1941  
Db |||||  
262 AAGTCAATAGACAAGTCACTTTTCAAGAGAAGGCTGGTTGTTGAAGAAAGACAA 321  
Qy 1942 GAGATCTCTGTTCTGTGATGCTGAAGTTGCTCTTGTGTCCTCCCATAGGGGAAA 2001  
Db |||||  
322 GAGATCTCTGTTCTGTGATGCTGAAGTTGCTCTCTCATTTTCTCTACTAAAGGCAAG 381  
Qy 2002 CTCTTCGAATACTCCACTGATCTTGGTAAGTCACTCAACTTCTTACTTTTAAAAAAT 2061  
Db |||||  
382 CTTTGTGAATACTCCAGCATCCTTGGTACGTTTCTTCTTCATATATATAGTTTATT 441  
Qy 2062 CTTTGAATCTGCTACTTTATAT 2083  
Db |||||  
442 TTATATATATATATATATAT 463

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Job time : 12360 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 18:51:28 ; Search time 328 Seconds  
(without alignments)

9082.245 Million cell updates/sec

Title: US-09-869-582-12

Perfect score: 5368  
Sequence: 1 gaattcccgatccata.....ttgggtcttcgcgcgatga 5368

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3148.2	58.6	4379	1	US-08-592-214A-17
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3	474.4	8.8	1865	1	US-08-592-214A-18
4	474.4	8.8	1865	3	US-09-149-976-18
5	390.4	7.3	2185	1	US-08-592-214A-19
6	390.4	7.3	2185	3	US-09-149-976-19
7	303.8	5.7	1054	2	US-08-576-156-1
8	303.8	5.7	1057	3	US-08-659-188-1
9	303.8	5.7	1057	3	US-08-655-227-1
10	303.8	5.7	1057	3	US-08-655-241-1
11	303.8	5.7	1057	4	US-09-398-326-1
12	285.8	5.3	1215	1	US-08-592-214A-1
13	285.8	5.3	1215	3	US-09-149-976-1
14	209.2	3.9	4816	1	US-08-592-214A-22
15	209.2	3.9	4816	3	US-09-149-976-22
16	188.2	3.5	794	1	US-08-592-214A-3
17	188.2	3.5	794	3	US-08-659-188-3
18	188.2	3.5	794	3	US-08-655-227-3
19	188.2	3.5	794	3	US-08-655-241-3
20	188.2	3.5	794	3	US-09-149-976-3
21	188.2	3.5	794	4	US-09-398-326-3
22	174.4	3.2	5855	1	US-08-592-214A-20
23	174.4	3.2	5855	3	US-09-149-976-20
24	173.8	3.2	768	1	US-08-592-214A-5
25	173.8	3.2	768	3	US-08-659-188-5
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27	173.8	3.2	768	3	US-08-655-241-5

28 173.8 3.2 768 3 US-09-149-976-5  
29 173.8 3.2 768 4 US-09-398-326-5  
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31 163.4 3.0 779 3 US-08-659-188-9  
32 163.4 3.0 779 3 US-08-655-227-9  
33 163.4 3.0 779 3 US-08-655-241-9  
34 163.4 3.0 779 3 US-09-149-976-9  
35 163.4 3.0 779 4 US-09-398-326-9  
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37 156.2 2.9 756 3 US-08-659-188-13  
38 156.2 2.9 756 3 US-08-655-227-13  
39 156.2 2.9 756 3 US-08-655-241-13  
40 156.2 2.9 756 3 US-09-149-976-13  
41 156.2 2.9 756 4 US-09-398-326-13  
42 153 2.9 756 1 US-08-592-214A-11  
43 153 2.9 756 3 US-08-659-188-11  
44 153 2.9 756 3 US-08-655-227-11  
45 153 2.9 756 3 US-08-655-241-11

#### ALIGNMENTS

RESULT 1  
US-08-592-214A-17  
; Sequence 17, Application US/08592214A  
; Patent No. 5811536  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
; TITLE OF INVENTION: Genes and Methods of Using Same  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,214A  
; FILING DATE: 26-JAN-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1927  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4379 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2095..2098  
; OTHER INFORMATION: /note= "N = one or more  
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; FEATURE:  
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; OTHER INFORMATION: /note= "sequence = Arabidopsis  
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US-08-592-214A-17





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## RESULT 2

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; Sequence 17, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; CITY: San Diego
; STREET: 4370 La Jolla Village Drive, Suite 700
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2095..2098
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
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; OTHER INFORMATION: /note= "sequence = Arabidopsis
; OTHER INFORMATION: thaliana API gene"
US-09-149-976-17
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Matches 4301; Conservative 0; Mismatches 7; Indels 1061; Gaps 9;
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Db 1260 TGGCCA-TATATGCTCTCCCTCCACCCCGCAGCAGCATCAATCCAGCATCTTACAT 1318  
Qy 4806 GCTCTCTCATAGCCATCTCTTTTCTCAAGTGGGTAAACAAAAATTAATCAATCAGTC 4865  
Db 1319 GCTCTCTCATAGCCATCTCTTTTCTCAACATGGGTAGTTTAAATAATTCGTCTCT- 1374  
Qy 4866 TTAATTTAAAGCACATATGTTATGCAAGCTAGTGTAGGTGTTGTAATTTCAATGAA 4925  
Db 1375 CTTACTTTCAAGTCATATGTTATATATACAGATAGTTAGGTGTTATAGTCCAGTAG 1434  
Qy 4926 GTTATAGCTGTAGTATGTTTACATGATGCTAGATTTTGAACCTAGAAAACTTTATTTT 4985  
Db 1435 TTAGGTTGTGTAGTATGTTTATGATGCTAGATTTGTAATTTCAAGTACTAAGATTTT 1494  
Qy 4986 AAAACAT-TATTTTATTAACGTAGTTTATGAAATGCTCGCAACAGCAAACTTATTA 5044  
Db 1495 CAGTTATATAATTAACGTATTGATCATCAATCAATGCTCGTAAAAAAACAGACTTATAT 1554

## RESULT 4

US-09-149-976-18  
; Sequence 18, Application US/09149976  
; Patent No. 6127123  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
; TITLE OF INVENTION: Genes and Methods of Using Same  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/149,976  
; FILING DATE: 09-SEP-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/592,214  
; FILING DATE: 26-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 3291  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1865 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 1077..1081  
; OTHER INFORMATION: /note="N = one or more  
; OTHER INFORMATION: nucleotides."

Qy 5045 GTGTGGAATAATGTACATGGAATGCTTGGAAAAAGCTAAGTCGACTTTTGTGTTG 5104  
Db 1555 TTTTGGGAAA--GTAGATGGAATGCTGCTAAAAGCTTAAGAAACCTTTGGGAGCAGGTC 1612  
Qy 5105 GTCTATG-----TGTTTAAGTACAATTTTAGTTTGTAGATAAATGAAATTAATATATCTT 5160  
Db 1613 GTATTTATGTTGTTCAATTAACCTTGAGGTAGTTAGATAAATACTATCTTTGATAT 1672  
Qy 5161 TGACATTTTCACAATGGAGCTGATATTTGATTTTCCCTTTGTTGACGGTGAACAATATGAT 5220  
Db 1673 GGCCTTTTACCAATTTTCACTACAAAACATGTGATATATTTTTCAGCAC- -TATGT 1722  
Qy 5221 ACATATGCACTTTCAT 5280  
Db 1723 AGATAATTTTGAAGCTAT 1782  
Qy 5281 AGATGATCCAATGGCAATGAGGAGGAATGATCTCGAATCGACTTTGAACCCGTTTACAA 5340  
Db 1783 AGAAGATCAATGGCAATGAGGAGGAACGATCTCGATCTCTCTTTGAACCCGTTTACAA 1842  
Qy 5341 CTGCAACCTTGGCTG 5355  
Db 1843 CTGCAACCTTGGCG 1857

[illegible]







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QY 4503 CATCTTACTAGCTCATATCTATGTATATGATATATAGACACTACTCCTTAATTAATAAT 4562
Db 1389 NNNCCCTACATTTGATGCTATTTATATATATATATATATATAGAGCTGCTGGCTTTGAAAT 1448
QY 4563 GTTATATAATGTTTCATTTGATGCTAGTGAACCTGCTGAAATAACTATTGTTACACCTATGATA 4622
Db 1449 GA-----TGATGATATGTTGATGATATGATATGATATGATATGATATGATATGATATG 1479
QY 4623 TATATAGTTTCTTCTACCTTTGAAATGATGATGATATATGTTGAAATTAATAATTTGCTG 4682
Db 1480 CAAACTGCTGTTGAAATGAACT-----TG 1506
QY 4683 GCAGATCAAGAGAGAGGAAATTTCTTAGGCTCAACAGGAGCTGGGATCAGCAGAA 4742
Db 1507 TCAGATTAAAGAGAGGAAACGTTCTTAGGGCGCAACAGAGCAATAGGGAGCAGCAGAA 1566
QY 4743 CCAAGGCCAAATATGCTCCCTCTGCTGACCGCAGCAGCAGCAAAATCCAGCATCTCTTA 4802
Db 1567 CCATGGCCATATATGCTCCGCTCCACCCCGCAGCAGCATCAATCCAGCATCTCTTA 1626
QY 4803 CATGCTCTCTCATCAGCATCTCTCTTTCTCAACATGGGGTAAACAAAATTAATAATCA 4862
Db 1627 CATGCTCTCTCATCAGCATCTCTCTTTCTCAACATGGGGTAAATTAATAAT---TCGTT 1683
QY 4863 GTCTTAATTTAAAGCAGATATGTTATGCA-AGCTAGTTAGCTTGGTGTGTTGTTTCAAT 4921
Db 1684 CTCTTACTTTCAAGTACATATGTTTATATATATCAAGATAGTTAGGTTTATAGTCCAG 1743
QY 4922 TGAAGTTATAGCTGTTAGTATGATGTTACATGCTAGATTTTGAACCTAGAAAATCTTTA 4981
Db 1744 TGAGTTAAGTTGTTAGTATGATGTTAGATG--TCTAATTTGTAATACAACTACTAAG 1801
QY 4982 TTTTAAACATATTTTATTAACGTA-----GTTAATGCAATGGTGGCAACAGCAACAA 5036
Db 1802 ATTTTTCATGATATATTTAAAGCTATTAATCATCAATCAATGGTGGTAAAGAAACAG 1861
QY 5037 ACTTATAGTGGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5095
Db 1862 ACTTATATTTTGGGAAA-GTAGATGGAATGCTGCTAAAGCTTAAGAAACCTTTGGG 1920
QY 5096 ---TTGTTGTTGCTATGTTTAACTACAAATTTTGTAGTAAATGAATTAAT 5152
Db 1921 AGCAGGCTGTTTATGTTGTTCAATTAATGATGATGATGATGATGATGATGATGATGATG 1980
QY 5153 TATATCTTTGACATTTTCAATGAGCTGATGATGATGATGATGATGATGATGATGATGATG 5212
Db 1981 TTTGATATGGGCTTTACCAATTTCACTACAAACA-TGTGATATTTTCAGCACCTATGT 2039
QY 5213 ATATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5272
Db 2040 AGATAATTTTGTAGGCTATATCATGTGCA-----TATGAATGTAATGATGAGGGCTG 2092
QY 5273 TATCAAGAGATGATCCAAATGGCAATGAGGAGGATGATGATGATGATGATGATGATGATG 5332
Db 2093 TATCAAGAGAGATCAATGGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2152
QY 5333 GTTTTCAACTGCAACCTTGGCTG 5355
Db 2153 GTTTTCAACTGCAACCTTGGCCG 2175

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RESULT 6

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; us-09-149-976-19
; Sequence 19, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700

```

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; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2185 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1389..1391
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1389..1391
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2185
; OTHER INFORMATION: /note= "sequence = Brassica
; OTHER INFORMATION: oleracea var. botrytis AP1 gene"
; US-09-149-976-19
; Query Match 7.3%; Score 390.4; DB 3; Length 2185;
; Best Local Similarity 59.4%; Pred. No. 1.1e-88; Indels 367; Gaps 21;
; Matches 1262; Conservative 0; Mismatches 494;
; QY 3300 TATTTATATAATAAAATGATAATTGGTTGATGATA--AAGCTAACCTTAATTTCTGTGAAA 3357
; Db 353 TATGATATAATATGATCATAAATTTGTTGATGATAAGAGCTAGCCCTAATTTCTGTGAAT 412
; QY 3358 TGATCAGTATGGAGAAGATACCTTGAACGGTATGAGAGGTAAGCTTCTAGCGGAAAGACAGC 3417
; Db 413 TGAACAGTATGGAGGAGATACCTTGAACGGTATGAGAGATCTCTTACGCGAGAGACAGC 472
; QY 3418 TTATTCACCTGAGTCCGAGCTCAATGTTTCAATAAATATTTCTCTCTTATTAATCCACA 3477
; Db 473 TTATAGCCTGAGTCCGAGCTCAATGTTTCAATAAATTTCTCTCTTATTAATTAAT 532
; QY 3478 TATATATTATATCAATCTATTGTTAGTATGATGAATTTTATTTGTATAAACTCTCTGGT 3537
; Db 533 TAAATATTATTTTCAATTTAGTATATAT-----ACTTATCTGTATTAACCTTGTGAG 585
; QY 3538 ACACAGCAAACTGGTCGATGGAGTATAACAGCTTAAAGCTTAAGATGAGCTTTTGGAG 3597
; Db 586 ATATAGCAAACTGGTCGATGGAGTATAAGCTTAAAGCTTAAGATGAGCTTTTGGAG 645
; QY 3598 AGAACCAGAGGTACACATTACCTCATCACATTTCTATCTAGAAA-ATCGATCGGTT 3656

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; FILING DATE: 12-21-95
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,336
; FILING DATE: 12-21-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REFERENCE/DOCKET NUMBER: 07251/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1054
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-576-156-1

Query Match 5.7%; Score 303.8; DB 2; Length 1054;
Best Local Similarity 99.3%; Pred. No. 1.5e-51;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 TTCCCTAATTGGTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 1780
Db 2 TTTCCTAATTGGTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 61

QY 1781 TTGGGGGCTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAGGATCAA 1840
Db 62 TTGGGGGCTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAGGATCAA 121

QY 1841 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTGA 1900
Db 122 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTGA 181

QY 1901 CATTTCTGAAAAGAGAGCTGGTCTTTTGAAGAACTCATGAGATCTCTGTCTCTGTG 1960
Db 182 CATTTCTGAAAAGAGAGCTGGTCTTTTGAAGAACTCATGAGATCTCTGTCTCTGTG 241

QY 1961 ATGCTGAAGTGTCTTTGTTGTTCTCTCCCATAAAGGGGAACTCTTCGAATACTCCACTG 2020
Db 242 ATGCTGAAGTGTCTTTGTTGTTCTCTCCCATAAAGGGGAACTCTTCGAATACTCCACTG 301

QY 2021 ATTCCTG 2027
Db 302 ATTCCTG 308

RESULT 8
US-08-659-188-1
; Sequence 1, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996

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; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..893
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1057
; OTHER INFORMATION: /note= "product = Arabidopsis
; OTHER INFORMATION: thaliana API."
;
US-08-659-188-1

Query Match 5.7%; Score 303.8; DB 3; Length 1057;
Best Local Similarity 99.3%; Pred. No. 1.5e-51;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 TTCTTAATTGGTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 1780
Db 2 TTTCCTAATTGGTTCATACCAAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 61

QY 1781 TTGGGGGCTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAGGATCAA 1840
Db 62 TTGGGGGCTCTTTGTTTGGTCTTTTAGAGTAAGAGTTTCTTAAAAAGGATCAA 121

QY 1841 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTGA 1900
Db 122 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTGA 181

QY 1901 CATTTCTGAAAAGAGAGCTGGTCTTTTGAAGAACTCATGAGATCTCTGTCTCTGTG 1960
Db 182 CATTTCTGAAAAGAGAGCTGGTCTTTTGAAGAACTCATGAGATCTCTGTCTCTGTG 241

QY 1961 ATGCTGAAGTGTCTTTGTTGTTCTCTCCCATAAAGGGGAACTCTTCGAATACTCCACTG 2020
Db 242 ATGCTGAAGTGTCTTTGTTGTTCTCTCCCATAAAGGGGAACTCTTCGAATACTCCACTG 301

QY 2021 ATTCCTG 2027
Db 302 ATTCCTG 308

RESULT 9
US-08-655-227-1
; Sequence 1, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996

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STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/398,326  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/659,188  
FILING DATE: 05-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 3739  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1057 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 124..893  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..1057  
OTHER INFORMATION: /note= "product = Arabidopsis  
US-09-398-326-1

Query Match 5.7%; Score 303.8; DB 4; Length 1057;  
Best Local Similarity 99.3%; Pred. No. 1.5e-51;  
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 TTCTAATTGGTTCATACCAAGCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 1780  
Db 2 TTTCCAATTGGTTCATACCAAGCTGAGCTCTCTTTATATCTCTCTGTAGTTCTTA 61

QY 1781 TTGGGGGCTTTGTTTGTGTTCTTTTAGAGTAAGAGTTTCTTAAAGAGGATCA 1840  
Db 62 TTGGGGGCTTTGTTTGTGTTCTTTTAGAGTAAGAGTTTCTTAAAGAGGATCA 121

QY 1841 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGCAAGATCAATAGACAAGTGA 1900  
Db 122 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGGATAGAGCAAGATCAATAGACAAGTGA 181

QY 1901 CATTTCTGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTGTG 1960  
Db 182 CATTTCTGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTGTG 241

QY 1961 ATGCTGAAGTGTCTGTGTGCTCTCCCATAGGGGAACCTCTCGAATACCTCCACTG 2020  
Db 242 ATGCTGAAGTGTCTGTGTGCTCTCCCATAGGGGAACCTCTCGAATACCTCCACTG 301

QY 2021 ATTCTTTG 2027  
Db 302 ATTCTTG 308

RESULT 12  
US-08-592-214A-1  
; Sequence 1, Application US/08592214A  
; Patent No. 5811536

GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
TITLE OF INVENTION: Genes and Methods of Using Same  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,214A  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1927  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1215 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(141..905, 909..971, 975..1047)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..1215  
OTHER INFORMATION: /note= "product = Arabidopsis  
OTHER INFORMATION: thaliana API"  
US-08-592-214A-1

Query Match 5.3%; Score 285.8; DB 1; Length 1215;  
Best Local Similarity 99.3%; Pred. No. 6e-48;  
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1739 CAAAGCTGAGCTCTCTTTATATCTCTCTAGTTCTTATTTGGGGCTCTTTGTTTG 1798  
Db 37 CGAAGCTGAGCTCTCTTTATATCTCTCTAGTTCTTATTTGGGGCTCTTTGTTTG 96

QY 1799 TTTGGTTCTTTTAGAGTAAGAGTTTCTTAAAGAGATCAAAATGGGAAGGGTAGGG 1858  
Db 97 TTTGGTTCTTTTAGAGTAAGAGTTTCTTAAAGAGATCAAAATGGGAAGGGTAGGG 156

QY 1859 TTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTCAATCTCGAAAAGAGAG 1918  
Db 157 TTCAATTGAAGAGGATAGAGAACAGATCAATAGACAAGTCAATCTCGAAAAGAGAG 216

QY 1919 CTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTCTGTGATGCTGAAGTTGCTTTG 1978  
Db 217 CTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTCTGTGATGCTGAAGTTGCTTTG 276

QY 1979 TTGTCTTCTCCCATAGGGGAAACTCTTCCGAAATCTCCCACTGATTTCTTG 2027  
Db 277 TTGTCTTCTCCCATAGGGGAAACTCTTCCGAAATCTCCCACTGATTTCTTG 325

RESULT 13  
US-09-149-976-1  
; Sequence 1, Application US/09149976

Patent No. 6127123  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
TITLE OF INVENTION: Genes and Methods of Using Same  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/149,976  
FILING DATE: 09-SEP-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/592,214  
FILING DATE: 26-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 3291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1215 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(141..905, 909..971, 975..1047)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..1215  
OTHER INFORMATION: /note= "product = Arabidopsis  
OTHER INFORMATION: thaliana APl"  
US-09-149-976-1

Query Match 5.3%; Score 285.8; DB 3; Length 1215;  
Best Local Similarity 99.3%; Pred. No. 6e-48;  
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1739 CAAGTCTGAGCTCTCTTTATATCTCTCTGTGATTTCTTATTTGGGGGCTTTGTTTG 1798  
Db 37 CGAAGTCTGAGCTCTCTTTATATCTCTCTGTGATTTCTTATTTGGGGGCTTTGTTTG 96  
Qy 1799 TTTCGTTCTTTTACAGTAAGAGTTTCTTAAAGAGATCAAAATCGGAGGGGTAGG 1858  
Db 97 TTTCGTTCTTTTACAGTAAGAGTTTCTTAAAGAGATCAAAATCGGAGGGGTAGG 156  
Qy 1859 TTCAATTGAAGAGGATAGAACAAAGATCAATAGCAAGTGCATCTTCGAAAAAGAGAG 1918  
Db 157 TTCAATTGAAGAGGATAGAACAAAGATCAATAGCAAGTGCATCTTCGAAAAAGAGAG 216  
Qy 1919 CTGCTCTTTTCAAGAAAGCTCATGATCTCTGTCTCTGTGATGCTGAAGTTGCTCTTG 1978  
Db 217 CTGCTCTTTTCAAGAAAGCTCATGATCTCTGTCTCTGTGATGCTGAAGTTGCTCTTG 276  
Qy 1979 TTGCTCTCTCCATAAGGGGAAACTCTTCGAATACTCCACTGATTTCTTG 2027  
Db 277 TTGCTCTCTCCATAAGGGGAAACTCTTCGAATACTCCACTGATTTCTTG 325

RESULT 14  
US-08-592-214A-22  
Sequence 22, Application US/08592214A  
Patent No. 5811536  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
TITLE OF INVENTION: Genes and Methods of Using Same  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,214A  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1927  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4816 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
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NAME/KEY: unsure  
LOCATION: 700..709  
OTHER INFORMATION: /note= "N = one or more  
OTHER INFORMATION: nucleotides."  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 3846..3853  
OTHER INFORMATION: /note= "N = one or more  
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NAME/KEY: unsure  
LOCATION: 4545..4548  
OTHER INFORMATION: /note= "N = one or more  
OTHER INFORMATION: nucleotides."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..4816  
OTHER INFORMATION: /note= "sequence = Brassica  
OTHER INFORMATION: oleracea var. botrytis CAL gene"  
US-08-592-214A-22

Query Match 3.9%; Score 209.2; DB 1; Length 4816;  
Best Local Similarity 64.1%; Pred. No. 1.5e-32;  
Matches 400; Conservative 0; Mismatches 208; Indels 16; Gaps 5;  
Qy 1538 ATTAGTACGAGATATACCAATGAGAGTCGACGCAAAATCCTAAAGAAACCACTGTGGT 1597  
Db 742 ATGAAGTCCAGTCAGACCAATGAGAGTCGACGCAAAATCCTAGTAAACTACTCTCTTT 801  
Qy 1598 TTTTGCACAAAGAGAAACCACTTTAGCTTTTCCCTAAACCACTCTTACCCA--AATC 1655  
Db 802 TATCCTTGTCCA---AAACCAGCTTTAGGTTTCCCTGAAACCGCTTATCCAAACATCT 858



Qy 2131 ACTACTGCTTTTGTATATATTT 2154  
| | | | |  
Db 1333 TATGAATTCACAAATTTGT 1356

Search completed: October 1, 2004, 04:33:58  
Job time : 382 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 17:32:03 ; Search time 1839 Seconds  
(without alignments)  
12400.395 Million cell updates/sec

Title: US-09-869-582-12  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002s:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5368	100.0	5368	3	AA15015 Nucleotid
2	3148.2	58.6	4379	2	AAV58318 Arabidops
3	3148.2	58.6	4379	3	AAC61415 Genomic D
4	3142.6	58.5	4375	2	AAT76892 Arabidops
5	1790.4	33.4	1838	6	AA142830 Arabidops
6	474.4	8.8	1865	2	AAV58319 Brassica
7	474.4	8.8	1865	3	AAC61416 Genomic D
8	470.4	8.8	1860	2	AAT76893 Brassica
9	390.4	7.3	2185	2	AAV58320 Brassica
10	390.4	7.3	2185	3	AAC61417 Genomic D
11	387.8	7.2	2179	2	AAT76894 Cauliflow
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14	311.4	5.8	1220	3	AA15016 cDNA enco
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17	303.8	5.7	1057	2	AAV02760 Arabidops
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22	285.8	5.3	1215	3	AAC61407 cDNA enco
23	245.8	4.6	1037	2	AAV81351 Arabidops

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25	209.2	3.9	4816	2	AAV58305	Aav58305 Brassica
26	209.2	3.9	4816	3	AAC61420	Aac61420 Genomic D
27	188.2	3.5	794	2	AAT76886	Aat76886 Brassica
28	188.2	3.5	794	2	AAV58316	Aav58316 Brassica
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33	188.2	3.5	794	3	AAC61408	Aac61408 cDNA enco
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37	174.4	3.2	5750	2	AAT76895	Aat76895 Arabidops
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40	173.8	3.2	768	2	AAT76887	Aat76887 Cauliflow
41	173.8	3.2	768	2	AAV58317	Aav58317 Brassica
42	173.8	3.2	768	2	AAT86630	Aat86630 APETALA1
43	173.8	3.2	768	2	AAV06020	Aav06020 Cauliflow
44	173.8	3.2	768	2	AAV02762	Aav02762 Cauliflow
45	173.8	3.2	768	3	AAZ57056	Aaz57056 B. olerac

## ALIGNMENTS

RESULT 1  
AAA15015  
ID AAA15015 standard; DNA; 5368 BP.  
XX  
AC AAA15015;  
XX  
DT 21-AUG-2000 (first entry)  
XX  
DE Nucleotide sequence of Arabidopsis AP1 promoter.  
XX  
KW AP1 promoter; transgenic plant; suppressed flowering;  
KW floral organ selective regulatory element; wood; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN W0200023578-A2.  
XX  
PD 27-APR-2000.  
XX  
PF 15-OCT-1999; 99WO-US024407.  
XX  
PR 16-OCT-1998; 98US-0104604P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Yanofsky MF;  
DR WPI; 2000-339680/29.  
XX  
PT Transgenic plants in which flowering is suppressed by a tissue specific  
PT cytotoxic gene product, useful for the production of wood for use as  
XX lumber or pulp.  
XX  
PS Claim 29; Fig 6a-f; 79pp; English.  
XX  
CC The present sequence represents the Arabidopsis AP1 promoter. The  
CC promoter is used to produce transgenic plants of the invention, which are  
CC characterized by suppressed flowering. The plants are transformed with a  
CC construct comprising a floral organ selective regulatory element (e.g.  
CC present sequence), operatively linked to a nucleotide sequence encoding a  
CC cytotoxic gene product (which is inheritable by the progeny). The plants  
CC may be grown for either human consumption or for use as a raw material in  
CC industry. When trees, they are particularly suitable for cultivation to  
CC provide wood. As the flowering process consumes 20-35% of the energy of a  
CC typical plant, it is advantageous to suppress flowering in order to  
CC improve wood and lumber yields. Suppression of flowering may be desired



[illegible]

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Db	3181	TTATAAAGGTATCATAGAGATCGGTACTTGATTGTGTATAGAGAAATCTCGTTTAAATGCG	3240
Qy	3241	ATAAAAACCATATAGATTATCTTAAATGTGATGATATTTTGGTCACATCTCCCATATT	3300
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Qy	3301	ATTATATATAATAATGATATTTGGTTGATGATAAAGCTAACCCCTAATTCCTGTGAAATGA	3360
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Qy	3421	TTGCACCTGAGTCCGACGTCAATGTATTTCAATAAATATTTCTCTTTTAAATCCACATAT	3480
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Qy	3541	CAGACAACTGGTGCATGGAGTATAACAGAGCTTTAAGGCTAAGATTGAGCTTTTGGAGAGA	3600
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Db	3961	GTTATGTTGTATTTTAAAGACTCCATATTTCTTAAAGTAATGGTGTGTTAATGTTGATG	4020
Qy	4021	TGTGTGATTCAGAACCAACTTATGTACGAGTCCATCAATGAGCTCCAAAAAAGGTATG	4080
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Db	4141	GTCCGCTTTCGGAATATGACAGGAGAGGCCATACAGGAGCAAAACAGCATGCTTTTCTTAAA	4200
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Db 2544 AAACGAGAGGTACACATTTACACTCATCACATTTCTATCTAGAAAAATCGATCGGGTTCCA 2603  
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Db 2844 AATATATATATCAGTAACTCAATATCAATTTTCATATGCTCTATAGGTTGGTTCCGAATGATG 2903  
QY 3960 AGTTATGTTGTATTTTAAAGACTCCATATTTAAAGTAAATGGGTTGTTTAAATGTTGAT 4019  
Db 2904 AGTTATGTTGTATTTTAAAGACTCCATATTTAAAGTAAATGGGTTGTTTAAATGTTGAT 2963  
QY 4020 GTGTGTATGCGAAGCAACTTATGTACGAGTCCATCAATGAGCTCCAAAAAAGGAT 4079  
Db 2964 GTGTGTATGCGAAGCAACTTATGTACGAGTCCATCAATGAGCTCCAAAAAAGGAT 3023  
QY 4080 GTAAAAACCCCTATCAAAATGTATGCTTATACAGAAACGTATAGGAACCTTAATTAACAAAT 4139  
Db 3024 GTAAAAACCCCTATCAAAATGTATGCTTATAGGAACCTTAATTAACAAAT 3083  
QY 4140 CGTCCGCTTTCCGAAATGACAGGAGAGCCCATACAGGAGCAAAACAGCAGCTTTCTTAA 4199  
Db 3084 CGTCCGCTTTCCG - AATGACAGGAGAGGCCCATACAGGAGCAAAACAGCAGCTTTCTTAA 3142  
QY 4200 ACAGGTAACACATGTCAATCATTTCTTTTGAACATGATGTTGTCATGCTATCTGTTA 4259  
Db 3143 ACAGG - AACACATGTCAATCATTTCTTTTCAACATGTTTGTCCATTTGCTATCTGTTA 3201  
QY 4260 CTTTCCACTGTTCTGCTCCACACTTCCAGCAAGCTATACCTAGCATATCTTCATATCTC 4319  
Db 3202 CTTTCCACTGTTCTGCTCCACACTTCCAGCAAGCTATACCTAGCATATCTTCATATCTC 3261  
QY 4320 CACTTAACTTCGGCACCATTAAATAAAAAATAGAAAAATCTTTGCAAAATTTGTTGAAATAG 4379  
Db 3262 CACTTAACTTCGGCACCATTAAATAAAAAATAGAAAAATCTTTGCAAAATTTGTTGAAATAG 3321  
QY 4380 CATAGATGTTGTCTATTGATGATATAATACACAGCCTGTACGATAGATATGTTGTCGG 4439  
Db 3322 CATAGATGTTGTCTATTGATGATATAATACACAGCCTGTACGATAGATATGTTGTCGG 3381  
QY 4440 TTTAGTTTAAAGGTGCTCTCGGATGAAAAATATTTTGAATCTTTTGAATGTTTGTCC 4499  
Db 3382 TTTAGTTTAAAGGTGCTCTCGGATGAAAAATATTTTGAATCTTTTGAATGTTTGTCC 3441  
QY 4500 CATCATTTCTTACTTAGCTCATATCTATGATATGAATATAGACACTACTCTCTAATTAATA 4559  
Db 3442 CATCATTTCTTACTTAGCTCATATCTATGATATGAATATAGACACTACTCTCTAATTAATA 3501  
QY 4560 AATGTTATATAGTTCATTCGATGAGTCAACTGTGAAAAATTAACATATTGTAACCAATGC 4619  
Db 3502 AATGTTATATAGTTCATTCGATGAGTCAACTGTGAAAAATTAACATATTGTAACCAATGC 3561  
QY 4620 ATATATATAGTTCCTTCACTTTTGAATTTGATGATGATAATATGCTTTGAAATTAATTTG 4679  
Db 3562 ATATATATAGTTCCTTCACTTTGAAATTTGATGATGATAATATGCTTTGAAATTAATTTG 3621  
QY 4680 CTGSCAGATCAAGGAGAGGAAAAATTTCTTTPAGGGCTCAACAGGAGCAGTGGGATTCAGA 4739





Db 720 GGGTTTTTTCACACTTGAAGTCTCAAAAAGAGAAAACTATTACAACGGAAAAATTCATTGTA 779  
Qy 781 AAAGAAAGTAAATTAAGCAAAATGAGCAAAAGGTTTTATGTGGTTTTATTTTCATTATATGATT 840  
Db 780 AAAGAAAGTAAATTAAGCAAAATGAGCAAAAGGTTTTATGTGGTTTTATTTTCATTATATGATT 839  
Qy 841 GACATCAAAATGATATATATGTGGTGGTTTTATTTAAACAATATATATGAGTATAAAGCTACA 900  
Db 840 GACATCAAAATGATATATATGTGGTGGTTTTATTTAAACAATATATATGAGTATAAAGCTACA 899  
Qy 901 AACTAAATATGTTGATGACGAAAAAATAATATATGTATGTATGTTGATTAACAACATAGCAC 960  
Db 900 AACTAAATATGTTGATGACGAAAAAATAATATATGTATGTATGTTGATTAACAACATAGCAC 959  
Qy 961 ATATTCAACTGATTTTTGTCCTGATCACTACAACCTTAATAGAACACACACACATTTGAAA 1020  
Db 960 ATA-TCAACTGATTTTTGTCCTGATCACTACAACCTTAATAGAACACACACACATTTGAAA 1018  
Qy 1021 AAATCTTTGACAAAACTATTTTTGGGTTTTGAAATTTTTGAATACTTACAATTTATCTTC 1080  
Db 1019 AAATCTTTGACAAAACTATTTTTGGGTTTTGAAATTTTTGAATACTTACAATTTA-TC TTC 1077  
Qy 1081 TCGATCTCTCTCTCTTCTTAAATCCGCGTACAAATCCGTCGACGCAATACATTACAC 1140  
Db 1078 TCGATCTCTCTCTCTTCTTAAATCCGCGTACAAATCCGTCGACGCAATACATTACAC 1137  
Qy 1141 AGTTGCTCAATTTGTTCTCAGCTCTACCAAAACATCTATGTCCAAAAGAAAGGCTCTATTT 1200  
Db 1138 AGTTGCTCAATTTGTTCTCAGCTCTACCAAAACATCTATGTCCAAAAGAAAGGCTCTATTT 1197  
Qy 1201 GTACTTCTACTGTTACAGCTGAGAACATTTAAATATATAAGCAAAATTTGATRAAAACAAAGG 1260  
Db 1198 GTACTTCTACTGTTACAGCTGAGAACATTTAAATATATAAGCAAAATTTGATRAAAACAAAGG 1257  
Qy 1261 GTTCTCACTTTATCCAAAGAAATAGTGTAAATAGGGTATAGAGAAATGTTTAATAAAA 1320  
Db 1258 GTTCTCACTTTATCCAAAGAAATAGTGTAAATAGGGTATAGAGAAATGTTTAATAAAA 1317  
Qy 1321 GGAAATTAATAATAGATATTTTGGTTT-GGTTTCAGATTTTTGTTTCGTAGATCTACAGGGAA 1379  
Db 1318 GGAAATTAATAATAGATATTTTGGTTTGGTTTCAGATTTTTGTTTCGTAGATCTACAGGGAA 1377  
Qy 1380 ATCTCCGGCGTCAATGCAAGCGAAGGTGACACTTTGGGGAAGGACCGAGTGGTCCGTACAA 1439  
Db 1378 ATCTCCGGCGTCAATGCAAGCGAAGGTGACACTTTGGGGAAGGACCGAGTGGT-CGTACAA 1436  
Qy 1440 TGTTACTTACCAATTTCTCTTCCAGAGAGTGCATTAATCAAAATGTTTATTTTCATATTT 1499  
Db 1437 TGTTACTTACCAATTTCTCTTCCAGAGAGTGCATTAATCAAAATGTTTATTTTCATATTT 1496  
Qy 1500 TTAAGTCCGCGAGTTTTATTTAAAAAATCATGGACCGGACATTTAGTACGAGATATACCAATG 1559  
Db 1497 TTAAGTCCGCGAGTTTTATTTAAAAAATCATGGACCGGACATTTAGTACGAGATATACCAATG 1556  
Qy 1560 AGAAGTCGACACGCAAAATCCTTAAGAAACCACTGTGGTTTTTGGCAAAACAAAGAAACCCAG 1619  
Db 1557 AGAAGTCGACACGCAAAATCCTTAAGAAACCACTGTGGTTTTTGGCAAAACAAAGAAACCCAG 1616  
Qy 1620 CTTTACGTTTTCCCTTAACCACTCTTACCCAAATCTCCCATTAATTAAGATCCCGAGA 1679  
Db 1617 CTTTACGTTTTCCCTTAACCACTCTTACCCAAATCTCTCCCATTAATTAAGATCCCGAGA 1676  
Qy 1680 CTCAACACACAGCTTTTTTATAAGGAAGAAAGAAAACTTTCCTAATTTGGTTTCATACC 1739  
Db 1677 CTCAACACAGCTTTTTTATAAGGAAGAAAGAAAACTTTCCTAATTTGGTTTCATACC 1736  
Qy 1740 AAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTTCTTATTTGGGGGTCTTTTGTGTGT 1799  
Db 1737 AAGTCTGAGCTCTCTTTATATCTCTCTGTAGTTTCTTATTTGGGGGTCTTTTGTGTGT 1796  
Qy 1800 TTGGTCTCTTTAGAGTAAGAGTTTTCTTAAGAAAGGATCAAAATGGGAAGGGGTAGGGT 1859  
Db 1797 TTGGTCTCTTTAGAGTAAGAGTTTTCTTAAGAAAGGATCAAAATGGGAAGGGGTAGGGT 1856

Qy 1860 TCAATTGAAGAGGATAGAGAAACAAGATCAATAGACAAGTGACATTTCTCGAAAAGAGAGC 1919  
Db 1857 TCAATTGAAGAGGATAGAGAAACAAGATCAATAGACAAGTGACATTTCTCGAAAAGAGAGC 1916  
Qy 1920 TGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTTCTGTGATGCTGAAGTTGCTCTTGT 1979  
Db 1917 TGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTCTTCTGTGATGCTGAAGTTGCTCTTGT 1976  
Qy 1980 TGTCTTCTCCCATAGAGGGAACCTTTCGAATATCTCACTGATTTCTTGGTAACTTCAACT 2039  
Db 1977 TGTCTTCTCCCATAGAGGGAACCTTTCGAATATCTTCCAACTGATTTCTTGGTAACTTCAACT 2036  
Qy 2040 AATCTTTTACTTTTTAAAAAATCTTTTAACTGTCTACTTTATATAGTTTTTTTTTCCCTT 2099  
Db 2037 AATCTTTTACTTTTTAAAAAATCTTTTAACTGTCTACTTTATATAGTTTTTTTTTCCCTT 2093  
Qy 2100 AAGTTGACTACTTGATTTGGCCCTAATTAATCACTACTGCTTTTGTATATATTTCTAGG 2159  
Db 2094 ----- 2093  
Qy 2160 GCTTCCATTTTGGATTTTTGATTAGCCAGAAAAATGTTTAAACAAATTTGTATAATT 2219  
Db 2094 ----- 2093  
Qy 2220 TAAAAATCAAAACTTTTAGGGCGGTAGTGAAGTGAACCCCTAGAAACACACAGATTATACCAT 2279  
Db 2094 ----- 2093  
Qy 2280 AGTAATTAACCTTGATATATTTGCAATATTTATCAGCATCATATCTTCAAACTCAAGAGA 2339  
Db 2094 ----- 2093  
Qy 2340 TATAGAACGGTATGTTAATCTTTGNACTAGGGTTTGTATCCCTAACTCATATGAATCCT 2399  
Db 2094 ----- 2093  
Qy 2400 TTTGTTCTCCAATAGCCATGTCTTTGCAATTTGCAGATCTAAGCTCTAATGTATGCCATA 2459  
Db 2094 ----- 2093  
Qy 2460 GTAAGAAAAAAGATCTGTAGTGTTCCTCGCTCACTGAGTTCGAGTTTTTAAATGAAGTG 2519  
Db 2094 ----- 2093  
Qy 2520 TCGTTTCTTTTTCATATATAGTTGCAACTGGAATTATAATTAATAAATAATATATGAGCAGA 2579  
Db 2094 ----- 2093  
Qy 2580 GAAAAATAATTTAAAAATAGATATAGATAACAATGTCAAAATGAGAAATTTTTTATTAGAAAG 2639  
Db 2094 ----- 2093  
Qy 2640 AATATTTAACTTACGAGTTGTTTTTTTTCAGCTGTAAAAAGAAATATCTAATTTGTTCTCNC 2699  
Db 2094 ----- 2093  
Qy 2700 GACTGTGCTTTCATGTTTTTGGCAAAATCTAAGCAAAAGAAAAATGTTTAAACTCGGATCTTAAG 2759  
Db 2094 ----- 2093  
Qy 2760 ATTATGAACCTGTAATATAAAACACTATATAGTATTAATTTTGAACACTAGTGTGCTTCTT 2819  
Db 2094 ----- 2093  
Qy 2820 TTGCTACTTTGACTTTTAGAAAAATTAACACTGAAACAAAGATGTCAAACTCTGAGTAGGAGT 2879  
Db 2094 ----- 2093  
Qy 2880 CTTTGACCTCTGGGATCCATAAAAAAGAACTAACTCCATCTTAAAAATCGGCTTCTTACCG 2939  
Db 2094 ----- 2093





Db 4042 TGTGGTCTATGTTTAAAGTACAAATTTAGTTGTTAGATAAATGAAATTAATATATCT 4101  
 QY 5160 TTGACATTTCAATGGAGTGAATTTGATTTTCCCTTTGTTGTTAGCGTGAACATATGAT 5219  
 Db 4102 TTGACATTTCAATGGAGTGAATTTGATTTTCCCTTTGTTGTTAGCGTGAACATATGAT 4161  
 QY 5220 TACATATGCACTTTCATATATATCTATGATGTTGTAATGCGAGTGTCTGTATCAAG 5279  
 Db 4162 TACATATGCACTTTCATATATATCTATGATGTTGTAATGCGAGTGTCTGTATCAAG 4221  
 QY 5280 AAGATGATCCAAATGGCAATGAGGAGGAATGATCTCGAACTGACTCTTGAACCCGTTTACA 5339  
 Db 4222 AAGATGATCCAAATGGCAATGAGGAGGAATGATCTCGAACTGACTCTTGAACCCGTTTACA 4281  
 QY 5340 ACTGCAACTTGGCTGCTTGGCCGATGA 5368  
 Db 4282 ACTGCAACTTGGCCG-TTGGCCGATGA 4309

## RESULT 4

AAAT76892

ID AAAT76892 standard; cDNA; 4375 BP.

XX

AC AAAT76892;

XX

DT 11-MAY-1998 (first entry)

XX

DE Arabidopsis floral meristem identity gene APETALA (AP1).

XX

KW Floral meristem identity gene; APETALA1; AP1 gene; flower development;  
 transgenic plant; angiosperm; ss.

XX

OS Arabidopsis thaliana.

XX

PN WO9727287-Al.

XX

PD 31-JUL-1997.

XX

PF 26-JAN-1996; 96WO-US001041.

XX

PR 26-JAN-1996; 96WO-US001041.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Yanofsky MF;

XX

DR WPI; 1997-393675/36.

XX

DR P-PSDB; AAW23811.

XX

PT Cauliflower floral meristem identity genes and related proteins - used to  
 develop products for converting shoot meristem to floral meristem and  
 promoting early flowering in an angiosperm.

XX

PS Disclosure; Fig 10A-F; 132pp; English.

XX

CC This sequence comprises Arabidopsis thaliana APETALA (AP1) gene, which  
 encodes a floral meristem identity gene product (see AAW23811) that is  
 involved in the conversion of shoot meristem to floral meristem. Mutation  
 of the AP1 gene results in replacement of a few basal flowers by  
 inflorescence shoots that are not subtended by flowers. When AP1 is  
 ectopically expressed in shoot meristem, the shoot meristem is converted  
 to floral meristem and early flowering can occur. The invention relates  
 to floral meristem identity genes AP1, LFY and especially CAL (see  
 AAT76885-97 and AAT99437) and their use in converting shoot meristem to  
 floral meristem and in promoting early flowering in transgenic plants,  
 especially angiosperms such as cereals, legumes, oilseed plants, trees,  
 fruit-bearing plants and ornamental flowers

XX

SQ Sequence 4375 BP; 1488 A; 707 C; 714 G; 1466 T; 0 U; 0 Other;

Query Match

Best Local Similarity 58.5%; Score 3142.6; DB 2; Length 4375;

Matches 4300; Conservative 0; Mismatches 4; Indels 1065; Gaps 9;

QY 1 GAAATCCCGGATCTCCATATACAT 60  
 Db 1 GAAATCCCGGATCTCCATATACAT 60  
 QY 61 ATTTCTCTATACACTATCTTTTAACTTATGTCGTTTCAAACCTCAGGACGTACATGTT 120  
 Db 61 ATTTCTCTATACACTATCTTTTAACTTATGTCGTTTCAAACCTCAGGACGTACATGTT 120  
 QY 121 TTAATTTGGTTATATAACCGACCATTTCAAGTATATATATATATATATATATATATATATATAT 180  
 Db 121 TTAATTTGGTTATATAACCGACCATTTCAAGTATATATATATATATATATATATATATATATAT 180  
 QY 181 AATATAAATCTTCTATCAAGAAATACATAAAGTTGATTAATAAATCAAGTGACATCTTTT 240  
 Db 181 AATATAAATCTTCTATCAAGAAATACATAAAGTTGATTAATAAATCAAGTGACATCTTTT 240  
 QY 241 AGCATAGGTTTCAATTTGGCATAGAAATATATAAATCTAAATGAATCTTAACTTAAATA 300  
 Db 241 AGCATAGGTTTCAATTTGGCATAGAAATATATAAATCTAAATGAATCTTAACTTAAATA 300  
 QY 301 GATTTTACTATATTAACAATTTTCTTTTACATGCTCTAATTTATTTTCTTAAATATAG 360  
 Db 301 GATTTTACTATATTAACAATTTTCTTTTACATGCTCTAATTTATTTTCTTAAATATAG 360  
 QY 361 TATGATTTGTTGTTTGGTGAACAATAATACCGTGAAGCAATAGTTGCTTAAAGATGTCCA 420  
 Db 361 TATGATTTGTTGTTTGGTGAACAATAATACCGTGAAGCAATAGTTGCTTAAAGATGTCCA 420  
 QY 421 AATATTTATAAATTAACAAGTAAATCAATTAAGGAAGAGACACCGTGGGAAAACACCAAT 480  
 Db 421 AATATTTATAAATTAACAAGTAAATCAATTAAGGAAGAGACACCGTGGGAAAACACCAAT 480  
 QY 481 AAGAGAAGAAATGGAAAAACAGAAAGAAATTTTAAACAAGAAATCAATTAAGTACCTC 540  
 Db 481 AAGAGAAGAAATGGAAAAACAGAAAGAAATTTTAAACAAGAAATCAATTAAGTACCTC 540  
 QY 541 AAACCTGAGATATTTAAAGTAAATCAACTAAACAGGAACACCTTGAACAAAGAAATTT 600  
 Db 541 AAACCTGAGATATTTAAAGTAAATCAACTAAACAGGAACACCTTGAACAAAGAAATTT 600  
 QY 540 AAACCTGAGATATTTAAAGTAAATCAACTAAACAGGAACACCTTGAACAAAGAAATTT 599  
 Db 540 AAACCTGAGATATTTAAAGTAAATCAACTAAACAGGAACACCTTGAACAAAGAAATTT 599  
 QY 601 GAAATGTGTCCTCAACTTTTCACTTAATATATATGTTTCTTAAGGCTTATGCAATATATG 660  
 Db 601 GAAATGTGTCCTCAACTTTTCACTTAATATATATGTTTCTTAAGGCTTATGCAATATATG 660  
 QY 661 CCTTAAGCAAAATGCCGAATCTGTTTTTTTTTTTCTTATGTTGATTTGCTGCAATATAG 720  
 Db 661 CCTTAAGCAAAATGCCGAATCTGTTTTTTTTTTTCTTATGTTGATTTGCTGCAATATAG 720  
 QY 721 GGGTTTTTTCACACTTGAAGATCTCAAAGAGAAAACTATTACAACGGAAATTCATTGTA 780  
 Db 721 GGGTTTTTTCACACTTGAAGATCTCAAAGAGAAAACTATTACAACGGAAATTCATTGTA 780  
 QY 781 AAAGAAGTGATTAAGCAAAATTCAGCAAAAGGTTTTTATGTTGTTTATTTCAATATATGATT 840  
 Db 781 AAAGAAGTGATTAAGCAAAATTCAGCAAAAGGTTTTTATGTTGTTTATTTCAATATATGATT 840  
 QY 841 GACATCAAAATTCATATATATATGTTGTTTATTTAAACATATATATGATATAACGTACA 900  
 Db 841 GACATCAAAATTCATATATATATGTTGTTTATTTAAACATATATATGATATAACGTACA 900  
 QY 840 GACATCAAAATTCATATATATGTTGTTTATTTAAACATATATATGATATAACGTACA 899  
 Db 840 GACATCAAAATTCATATATATGTTGTTTATTTAAACATATATATGATATAACGTACA 899  
 QY 901 AACTAAATATGTTTGAATGACGAAAAAATAATATGTTGTTGTTGATTAACAACATAGCAC 960  
 Db 901 AACTAAATATGTTTGAATGACGAAAAAATAATATGTTGTTGTTGATTAACAACATAGCAC 960  
 QY 961 ATATTCACATGATTTTGTGCTGATCATCTACAACCTTATATAGAACACACACATTTGAAA 1020  
 Db 961 ATATTCACATGATTTTGTGCTGATCATCTACAACCTTATATAGAACACACACATTTGAAA 1020  
 QY 960 ATA-TCAACTGATTTTGTCTGATCATCTACAACCTTATATAGAACACACACATTTGAAA 1018  
 Db 960 ATA-TCAACTGATTTTGTCTGATCATCTACAACCTTATATAGAACACACACATTTGAAA 1018  
 QY 1021 AAATCTTTGACAAAAATACTATTTTGGGTTTCAAAATTTTGAATTTTGAATTTTCTTCTC 1080  
 Db 1021 AAATCTTTGACAAAAATACTATTTTGGGTTTCAAAATTTTGAATTTTGAATTTTCTTCTC 1080  
 QY 1019 AAATCTTTGACAAAAATACTATTTTGGGTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTT 1077  
 Db 1019 AAATCTTTGACAAAAATACTATTTTGGGTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTT 1077

QY 1081 TCGATCTTCTCTCTCTTCTTAAATCCTGCGTACAAATCCGTCGACGCAATACATTACAC 1140  
Db |||||  
QY 1078 TCGATCTTCTCTCTCTTCTTAAATCCTGCGTACAAATCCGTCGACGCAATACATTACAC 1137  
Db |||||  
QY 1141 AGTTGTCAATGGTCTCTCAGCTCTACCAAAAACATCTATTGCCAAAAGAAAGGTCTATTT 1200  
Db |||||  
QY 1138 AGTTGTCAATGGTCTCTCAGCTCTACCAAAAACATCTATTGCCAAAAGAAAGGTCTATTT 1197  
QY 1201 GTACTTCAGCTTTACAGCTGAGACATTAATAATAAATAAGCAAAATTTGATAAAAAAGG 1260  
Db |||||  
QY 1198 GTACTTCAGCTTTACAGCTGAGACATTAATAATAAATAAGCAAAATTTGATAAAAAAGG 1257  
QY 1261 GTTCTCACCTTATCCAAAAGATAGTGAATAAGGTAAATAGAGAAATGTTAAATAAA 1320  
Db |||||  
QY 1258 GTTCTCACCTTATCCAAAAGATAGTGAATAAGGTAAATAGAGAAATGTTAAATAAA 1317  
QY 1321 GGAATTAATAATAGATATTTGGTT - GGTTTCAGATTTTGTTCGTAGATCTACAGGGAA 1379  
Db |||||  
QY 1318 GGAATTAATAATAGATATTTGGTTGGTTTCAGATTTTGTTCGTAGATCTACAGGGAA 1377  
QY 1380 ATCTCGCGCTCAATGCAAGCAAGGTGACACTTTGGGGAAGGACCGAGTGGTCCGTACAA 1439  
Db |||||  
QY 1378 ATCTCGCGCTCAATGCAAGCAAGGTGACACTTTGGGGAAGGACCGAGTGGT - CGTACAA 1436  
QY 1440 TGTACTTACCATTTCTCTTCACGAGACGTCGATAATCAAAATGTTTATTTTCATATTT 1499  
Db |||||  
QY 1437 TGTACTTACCATTTCTCTTCACGAGACGTCGATAATCAAAATGTTTATTTTCATATTT 1496  
QY 1500 TTAAGTCGCGAGTTTATTAATAAATCATGGACCCGACATTTAGTACGAGATATACCAATG 1559  
Db |||||  
QY 1497 TTAAGTCGCGAGTTTATTAATAAATCATGGACCCGACATTTAGTACGAGATATACCAATG 1556  
QY 1560 AGAAGTCGACGCAATCTTAAGAAACCACTGTGGTTTTCGAAACAAGAGAAACCAAG 1619  
Db |||||  
QY 1557 AGAAGTCGACGCAATCTTAAGAAACCACTGTGGTTTTCGAAACAAGAGAAACCAAG 1616  
QY 1620 CTTTAGCTTTTCCCTAAACCACTCTTACCAATCTCTCATAAATAAGATCCCGAGA 1679  
Db |||||  
QY 1617 CTTTAGCTTTTCCCTAAACCACTCTTACCAATCTCTCATAAATAAGATCCCGAGA 1676  
QY 1680 CTCAAACACAAGTCTTTTATAAGGAAAGAAAGAAACCTTCTTAATTTGGTTTCATACC 1739  
Db |||||  
QY 1677 CTCAAACACAAGTCTTTTATAAGGAAAGAAAGAAACCTTCTTAATTTGGTTTCATACC 1736  
QY 1740 AAGTCTGAGCTCTTCTTTATATCTCTCTGTAGTCTTCTTATGGGGTCTTTGTTTGT 1799  
Db |||||  
QY 1737 AAGTCTGAGCTCTTCTTTATATCTCTCTGTAGTCTTCTTATGGGGTCTTTGTTTGT 1796  
QY 1800 TTGTTCTTTTAGAGTAAGAGTTTCTTAAAGAGGATCAAAATGGAGGAGGTAGGGT 1859  
Db |||||  
QY 1797 TTGTTCTTTTAGAGTAAGAGTTTCTTAAAGAGGATCAAAATGGAGGAGGTAGGGT 1856  
QY 1860 TCAATTGAAGAGGTAGAGAACCAAGATCAATAGACAAGTGCATTTCTCGAAAGAAAGAGC 1919  
Db |||||  
QY 1857 TCAATTGAAGAGGTAGAGAACCAAGATCAATAGACAAGTGCATTTCTCGAAAGAAAGAGC 1916  
QY 1920 TGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTGATGCTGAAAGTGTCTTGT 1979  
Db |||||  
QY 1917 TGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTGATGCTGAAAGTGTCTTGT 1976  
QY 1980 TGTCTTCTCCCATAAAGGAAACCTTTTCGAATCTCCCACTGATTTCTGGTAACCTCAACT 2039  
Db |||||  
QY 1977 TGTCTTCTCCCATAAAGGAAACCTTTTCGAATCTCCCACTGATTTCTGGTAACCTCAACT 2036  
QY 2040 AATCTTTTACTTTTAAAAAATCTTTTAACTGCTACTTTTATATAGTTTTTTTCCCTT 2099  
Db |||||  
QY 2037 AATCTTTTACTTTTAAAAAATCTTTTAACTGCTACTTTTATATAGTTTTTTTCCCTT - 2094  
QY 2100 AAGTTGACTACTGATTTGCGCTAAATTTATCACTACTGCTTTTGTATATATTTTCTAGG 2159  
Db |||||  
QY 2095 - - - - - 2094  
QY 2160 GCITCCATTTTGGATTTTGTATTAGCCAGAAAAATGTTTAAATACAAAATTTGTATAATT 2219

Db 2095 - - - - - 2094  
QY 2220 TAAAAATCAAAACCTTTAGGCGCGTAGTGAAGTGAACCTAGAACACACAGATTATACCAT 2279  
Db 2095 - - - - - 2094  
QY 2280 AGTAATTTACCTTTGATATATTGTGCAATATTATTCAGCATCATATCTTCAAACTCAAGAGA 2339  
Db 2095 - - - - - 2094  
QY 2340 TATAGAAGGTATGTTAATCTTTGAACTAGGTTTTCATCCCTAACTCAATCAATCAATCT 2399  
Db 2095 - - - - - 2094  
QY 2400 TTTGTTCTCCAATAGCCATGCTTTTCGAATTTTCAGATCTAAGCTCTAATTTGATGCCATA 2459  
Db 2095 - - - - - 2094  
QY 2460 GTAAGAAAAATAAGATCTGTAGTTTTCACCTCGCTCACTGAGTTCGAGTTTAAATGAAGTG 2519  
Db 2095 - - - - - 2094  
QY 2520 TCGTTTCTTTTTCATATATAGTTGCAACTGGAATTATAATTAATAAATAATTTATCGGACGA 2579  
Db 2095 - - - - - 2094  
QY 2580 GAAAAATAATTTAAAAATAGATATAGATAACAATGTCAAAATTTGAGAAATTTTATTAGAAAG 2639  
Db 2095 - - - - - 2094  
QY 2640 AATATTTAACTTAGAGTGTGTTTTTTTTCAGCTGCTGTAAGAAATATCTAATTTGTTCTCAC 2699  
Db 2095 - - - - - 2094  
QY 2700 GACTGTGCTTTCATGTTTTCGAATCTAAGCAAGAAATAATGTTTAACTCGGATCTTAAG 2759  
Db 2095 - - - - - 2094  
QY 2760 ATTATGAACCTGTAATATAAAACACTATATAGTATTAAATTTGAACTAGTGTGCTCTT 2819  
Db 2095 - - - - - 2094  
QY 2820 TTGCTACTTTGACTTTAGAAATTTAAACTGAAACAAAGATGTCAAACTCTGAGTAGGAGT 2879  
Db 2095 - - - - - 2094  
QY 2880 CTTTGACCTCTGGGATCCATAAAAGAACTAACTCCATCCATAAAATCGGCTTCTTACC 2939  
Db 2095 - - - - - 2094  
QY 2940 ATGCTCAAACTTAGCTCCAAAGCAACAGCTGTTCTTCTTTTTTTTTTTTTTTTTTTTT 2999  
Db 2095 - - - - - 2094  
QY 3000 TTTTAAGCATTTGCTTGTCTGAAAGAAATAAGATTGGTAAATTTGGCAAGATTATAAT 3059  
Db 2095 - - - - - 2094  
QY 3060 AATTTATTAAATGTGTCGCACTAAGAGATTTTCTGTACTAATTTGTAGCAAAATTTAA 3119  
Db 2095 - - - - - 2094  
QY 3120 GAAACCGCATTTAGAACTGAAGCTAAGCATAGGCTCTATGATTCATACTGTTTGT 3179  
Db |||||  
QY 2095 - - - - - 2094  
QY 3180 ATTATAAGGTATCATAGAGATCGGTACTTGTATTGTTATAGGAAATCTTGGTTTAAATG 3239  
Db |||||  
QY 2120 ATTATAAGGTATCATAGAGATCGGTACTTGTATTGTTATAGGAAATCTTGGTTTAAATG 2179  
Db |||||  
QY 3240 CATAAACCATCATTTAGATTTTATCTTAAATGTGATGATTTTGGTCACTCTCCATAT 3299  
Db |||||

Db 2180 CATAAACCATCATTTAGATTTTATCTCTAAATGCTGATGATATTTTGGTCACATCTCCATAT 2239  
QY 3300 TATTTATATATAAATGATTAATTTGGTTGATGATTAAGCTTAACCTTAATTTCTGTGAATG 3359  
Db 2240 TATTTATATAAATGATTAATTTGGTTGATGATTAAGCTTAACCTTAATTTCTGTGAATG 2299  
QY 3360 ATCAGTATGGAAGAATCTTCAACGCTATGAGAGTCTCTTACGCGAAGAGACAGCTT 3419  
Db 2300 ATCAGTATGGAAGAATCTTCAACGCTATGAGAGTCTCTTACGCGAAGAGACAGCTT 2359  
QY 3420 ATTGCACCTGAGTCGAGCTCAATGTAATTTCAATAAATATTTCTCTTTTAAATCCACATA 3479  
Db 2360 ATTGCACCTGAGTCGAGCTCAATGTAATTTCAATAAATATTTCTCTTTTAAATCCACATA 2419  
QY 3480 TATATATATCAATCTATTTGATGATTAATGATGAAATTTTATTTGATTAATTTCTGTTTAC 3539  
Db 2420 TATATATATCAATCTATTTGATGATTAATGATGAAATTTTATTTGATTAATTTCTGTTTAC 2479  
QY 3540 ACAGACAAACTGGTCGATGGAGTATAACAGGCTTAAGGCTAAGATTGAGCTTTTGGAGAG 3599  
Db 2480 ACAGACAAACTGGTCGATGGAGTATAACAGGCTTAAGGCTAAGATTGAGCTTTTGGAGAG 2539  
QY 3600 AAACAGAGGTACATTTTACACTCATACATTTCTATCTAGAAATCGATCGGTTCCA 3659  
Db 2540 AAACAGAGGTACATTTTACACTCATACATTTCTATCTAGAAATCGATCGGTTCCA 2599  
QY 3660 TTTTAAAGTAAAGTTAAATTTCAATGCTATTTGAAATTCAGGCATTTCTTTGGGGAAGA 3719  
Db 2600 TTTTAAAGTAAAGTTAAATTTCAATGCTATTTGAAATTCAGGCATTTCTTTGGGGAAGA 2659  
QY 3720 CTTGCAAGCAATGAGCCCTTAAAGAGCTTCAGAAATCTGGAGCAGCAGCTTTGACACTGCTCT 3779  
Db 2660 CTTGCAAGCAATGAGCCCTTAAAGAGCTTCAGAAATCTGGAGCAGCAGCTTTGACACTGCTCT 2719  
QY 3780 TAAACATATCCGACTAGAAAAGTATGCTTCTGCTATTTCTGTTGAAATCATATCTATATA 3839  
Db 2720 TAAACATATCCGACTAGAAAAGTATGCTTCTGCTATTTCTGTTGAAATCATATCTATATA 2779  
QY 3840 ACTTAAAGCTTTACAGTGTATTAATTAATGTAAGTGAATTCAGGCATTTCTTTGGGGAAGA 3899  
Db 2780 ACTTAAAGCTTTACAGTGTATTAATTAATGTAAGTGAATTCAGGCATTTCTTTGGGGAAGA 2839  
QY 3900 AATATATATATCAGTAATCAATTTGATATCTCTATAGTGTGTTTGGTTCGAATGATG 3959  
Db 2840 AATATATATATCAGTAATCAATTTGATATCTCTATAGTGTGTTTGGTTCGAATGATG 2899  
QY 3960 AGTATGTTGTTATTTTAAAGTCTCATATTTCTTAAAGTAAATGAGTGTGTTTAAATGTTGAT 4019  
Db 2900 AGTATGTTGTTATTTTAAAGTCTCATATTTCTTAAAGTAAATGAGTGTGTTTAAATGTTGAT 2959  
QY 4020 GTGTGTTATGAGAACCACTTATGTCAGGTCCTATCATAGCTCCCAATTAAGGATG 4079  
Db 2960 GTGTGTTATGAGAACCACTTATGTCAGGTCCTATCATAGCTCCCAATTAAGGATG 3019  
QY 4080 GTAAACCCCTTATCAATGATGCTTATAGAGAAACGTTATAGGAAAGCTTAATTAACAAT 4139  
Db 3020 GTAAACCCCTTATCAATGATGCTTATAGAGAAACGTTATAGGAAAGCTTAATTAACAAT 3079  
QY 4140 CGTGGCTTTGGAATGACAGAGAGGCTTACAGAGGCTTACAGAGGCTTCTTCTTAA 4199  
Db 3080 CGTGGCTTTGCGG - AATGACAGAGAGGCTTACAGAGGCTTACAGAGGCTTCTTCTTAA 3138  
QY 4200 ACAGGTAACACATGTCATCTTTCTTTCTCATCAATGTTGTCATTTCTTCTTCTTCTTCTT 4259  
Db 3139 ACAGG - AACACATGTCATCTTTCTTTCTCATCAATGTTGTCATTTCTTCTTCTTCTTCTT 3197  
QY 4260 CCTTCCACTGTTCTGCTCCACACTTCCAGCCAGCTTATACCTACGATATCTTCTCATATCTC 4319  
Db 3198 CCTTCCACTGTTCTGCTCCACACTTCCAGCCAGCTTATACCTACGATATCTTCTCATATCTC 3257  
QY 4320 CACTTAACTCCGCACCATTAATAAATAGAAATCTTTCGAATTTGTTTGAATAG 4379  
Db 3258 CACTTAACTCCGCACCATTAATAAATAGAAATCTTTCGAATTTGTTTGAATAG 3317

QY 4380 CATAGATGTTGCTATTTGATTTGATATAATCACCAGCCTGCTAGTAGATATGTTTGTCCG 4439  
Db 3318 CATAGATGTTGCTATTTGATTTGATATAATCACCAGCCTGCTAGTAGATATGTTTGTCCG 3377  
QY 4440 TTTAGCTTTTAAAGTGTCTCTCGGATTGAAATPATTTTGAATCTTTTGAATGTTTGTCC 4499  
Db 3378 TTTAGCTTTTAAAGTGTCTCTCGGATTGAAATPATTTTGAATCTTTTGAATGTTTGTCC 3437  
QY 4500 CATATTTCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 4559  
Db 3438 CATATTTCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 3497  
QY 4560 AATGTTTAAATGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4619  
Db 3498 AATGTTTAAATGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3557  
QY 4620 ATATATATAGTTTCTTCACTTTTGAATTTGATGATGATGATGATGATGATGATGATGATG 4679  
Db 3558 ATATATATAGTTTCTTCACTTTTGAATTTGATGATGATGATGATGATGATGATGATGATG 3617  
QY 4680 CTGGCAGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4739  
Db 3618 CTGGCAGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3677  
QY 4740 GAACCAAGGCCAATATATGCTCTCCCTCTGCGACCGCAGCAGCAGCAGCAGCAGCAGCAG 4799  
Db 3678 GAACCAAGGCCAATATATGCTCTCCCTCTGCGACCGCAGCAGCAGCAGCAGCAGCAGCAG 3737  
QY 4800 TTACATGCTCTCTCATGAGCCTCTCTTTTCTCAACATGCGGTAAACAAAATTAATAA 4859  
Db 3738 TTACATGCTCTCTCATGAGCCTCTCTTTTCTCAACATGCGGTAAACAAAATTAATAA 3797  
QY 4860 TCAGTCTTAAATTTAAAGCAGATATGTCAGCTAGTTCAGTTCAGTTCAGTTCAGTTCAGT 4919  
Db 3798 TCAGTCTTAAATTTAAAGCAGATATGTCAGCTAGTTCAGTTCAGTTCAGTTCAGTTCAGT 3857  
QY 4920 ATTGAAGTTATAGCTGTTAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 4979  
Db 3858 ATTGAAGTTATAGCTGTTAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 3917  
QY 4980 TATTTTAAACATTTATTTTAAACATTTATTTTAAACATTTATTTTAAACATTTATTTTAAAC 5039  
Db 3918 TATTTTAAACATTTATTTTAAACATTTATTTTAAACATTTATTTTAAACATTTATTTTAAAC 3977  
QY 5040 TATTTAGTGGGAAATGTCATGCAATGCTTTCGGAAGCCTTAAGTCGACCTTTGTTGTTGTT 5099  
Db 3978 TATTTAGTGGGAAATGTCATGCAATGCTTTCGGAAGCCTTAAGTCGACCTTTGTTGTTGTT 4037  
QY 5100 TGTGCTCTATGTTGTTTAAAGTACAATTTTAAAGTACAATTTTAAAGTACAATTTTAAAGTACA 5159  
Db 4038 TGTGCTCTATGTTGTTTAAAGTACAATTTTAAAGTACAATTTTAAAGTACAATTTTAAAGTACA 4097  
QY 5160 TTTGACATTTCAATGAGGAGTATTTGATTTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5219  
Db 4098 TTTGACATTTCAATGAGGAGTATTTGATTTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4157  
QY 5220 TACATATGACCTTTCATATATATCTTATGATGATGATGATGATGATGATGATGATGATGATG 5279  
Db 4158 TACATATGACCTTTCATATATATCTTATGATGATGATGATGATGATGATGATGATGATGATG 4217  
QY 5280 AAGATGATCCAATGGCAATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 5339  
Db 4218 AAGATGATCCAATGGCAATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 4277  
QY 5340 ACTGCAACCTTGGCTTTCGCGCGATGA 5368  
Db 4278 ACTGCAACCTTGGCGG - TTCGCGCGATGA 4305

RESULT 5  
AAL42830  
ID AAL42830 standard; cDNA; 1838 BP.



Db 1378 TCTCCGCGTCAATCAAGCAAGGTGACACTCTGGGAGGACAGTGGTCCGTACAT 1437  
 QY 1441 GTTACTACCAATTTCTCTTCAAGAGAGTGCATTAATCAAAATGTTTATTTTCATATTTT 1500  
 Db 1438 GTTACTTACCAATTTCTCTTCAAGAGAGTGCATTAATCAAAATGTTTATTTTCATATTTT 1497  
 QY 1501 TAAAGTCGCGAGTTTATTAATAAATAATCATGGACCGACATTTAGTACGAGATATACCAATGA 1560  
 Db 1498 TAAAGTCGCGAGTTTATTAATAAATAATCATGGACCGACATTTAGTACGAGATATACCAATGA 1557  
 QY 1561 GAAGTCGACACCAATCTTAAAGAAACCACTGTGTGTTTTTGCACCAAGAGAAACCCAGC 1620  
 Db 1558 GAAGTCGACACCAATCTTAAAGAAACCACTGTGTGTTTTTGCACCAAGAGAAACCCAGC 1617  
 QY 1621 TTTAGCTTTTCCCTAAACCACTCTTACCAATCTCTCCATAAATAAAGATCCCGAGAC 1680  
 Db 1618 TTTAGCTTTTCCCTAAACCACTCTTACCAATCTCTCCATAAATAAAGATCCCGAGAC 1677  
 QY 1681 TCAAAACACAGTCTTTTATAAAGGAAGAAAGAAAGAAAGAAAGTCTTAAATGGTTTCATACCA 1740  
 Db 1678 TCAAAACACAGTCTTTTATAAAGGAAGAAAGAAAGAAAGAAAGTCTTAAATGGTTTCATACCA 1737  
 QY 1741 AAGTCTGAGCTCTCTTTATATCTCTCTTGTAGTTTCTTTATGGGGTCTTTGTTTGT 1800  
 Db 1738 AAGTCTGAGCTCTCTTTATATCTCTCTTGTAGTTTCTTTATGGGGTCTTTGTTTGT 1797  
 QY 1801 TGGTCTTTTAGAGTAAGATTTCTTAAAGGATCAA 1840  
 Db 1798 TGGTCTTTTAGAGTAAGATTTCTTAAAGGATCAA 1837

RESULT 6

AAV58319  
 ID AAV58319 standard; DNA; 1865 BP.  
 XX  
 AC AAV58319;  
 XX  
 DT 19-NOV-1998 (first entry)  
 XX  
 XX Brassica oleracea API gene.  
 DE  
 XX CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;  
 KW early flowering promotion; angiosperm; API gene; ds.  
 XX  
 OS Brassica oleracea.  
 XX  
 PN US5811536-A.  
 XX  
 PD 22-SEP-1998.  
 XX  
 PF 26-JAN-1996; 96US-00592214.  
 XX  
 PR 26-JAN-1996; 96US-00592214.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Yanofsky ME;  
 XX  
 DR WPI; 1998-530945/45.  
 XX  
 PT Cloned CAULIFLOWER genes - and vectors for converting shoot meristems to  
 PT floral meristems.  
 XX  
 PS Disclosure; Fig 11; 93pp; English.  
 XX  
 CC This sequence encodes the Brassica oleracea API protein. This sequence  
 CC was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER  
 CC (CAL) protein of the invention. An expression vector containing the CAL  
 CC DNA sequence can be used to convert shoot meristems to floral meristems,  
 CC especially to promote early flowering in angiosperms  
 XX  
 SQ Sequence 1865 BP; 610 A; 315 C; 339 G; 596 T; 0 U; 5 Other;

Query Match 8.8%; Score 474.4; DB 2; Length 1865;  
 Best Local Similarity 60.1%; Pred No. 8.5e-71;  
 Matches 1199; Conservative 0; Mismatches 596; Indels 200; Gaps 17;  
 QY 3423 GCACCTGAGTCGAGCTCAATGATATTTCAATAAATATTTCTCTCTTTTAAATCCACATATAT 3482  
 Db 1 GCACCTGAGTCGAGCTCAATGATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60  
 QY 3483 ATTATATCAATCTATTTGTAGTATTTGATGAATTTTATTTGTATATAAATCTTCTGGTACACA 3542  
 Db 61 ATTATTTTCAGTATTTAGTATATATA-----CTTATCTGTATTTAACTTTGAGATATA 113  
 QY 3543 GACAACTGGTCGATGGAGTATAACAGGCTTAAGGCTTAAGCTTAAGCTTTTGGAGAGAAA 3602  
 Db 114 GACGAACCTGGTCGATGGAGTATATAGGCTTAAGGCTTAAGCTTTTGGAGAGAAA 173  
 QY 3603 CCAGAGGTACACATT--TACACTCATCATTTCTTATCTAGAAAATCGATCGGGTCCAT 3660  
 Db 174 CCAGAGGTACATTTTCAATTCATTTATTAATAGATGAATATCAACAGGATTAAT 233  
 QY 3661 -----TTTAAAGTAAGTTAAATTT 3679  
 Db 234 GTTAGTTAAAAATGCATGATTTACTTTATAAGAAAATGATGATTTTAAATAACAAAAATG 293  
 QY 3680 CATTCATG--CTATTGAAATTCAGGCATTTCTTGGGGAAGACTTGCAGCAATGAGCCC 3737  
 Db 294 CATCATGCTCTATTGAAATTTAGGCATTTCTTGGGGAAGACTTGCAGCAATGAGCCC 353  
 QY 3738 TAAAGAGCTTCAGAAATCTGGACAGCAGCTTGCACACTGCTCTTAAAGCAGCATCCGACTAG 3797  
 Db 354 TAAAGAACTCCAGAACTTAGAGCAACAGCTTGATCTGCTCTTAAAGCAGCATCCGCTCTAG 413  
 QY 3798 AAAAGTATTCCTCTCTGCTATTTCTTGTGACATATCTATATTAACCTTAAAGCTTTACAAGT 3857  
 Db 414 AAAAGTATGAATCCTCTCTATTTCTTTAAATTAACATGTATACAACTTAAAC----- 463  
 QY 3858 GTTATTATAATGTGAACATTTGAAATACATATGTTGATGTATGATCAATATATATATATATAT 3917  
 Db 464 -----ACATATTTTATTATTTCAATACATATATATGATAGTACATAT 508  
 QY 3918 CAATATCAATTTGATATGCTATAGTGGTTGCGAATGTATAGTATATGTTGTATTTT 3977  
 Db 509 GTGATTTTATGTTGGATATAAAGATCAATCAGCTCGATTTAGATGT--ATGACTTTTTTA 567  
 QY 3978 AAGACTCCATATTTACTTAAAGTAATGGGTTGTTTAAATGTTGATGTGTGTATGCGAAGCC 4037  
 Db 568 AAGAAATTAGTATATAGATATGATTTAGTCAATGTAAATGTTGATGTTTATGCGAAGCC 627  
 QY 4038 AACTTATGTACGAGTCCATCAATGAGCTCCAAAAAAGGTATGTAAGAAACCCCTATCAAAAT 4097  
 Db 628 AACTTATGTACGACTCCATCAATGAGCTCCAAAGAAAGGTATGTAAGAAACCCCTATCAAAAT 687  
 QY 4098 GTATGCTTTATAGAGAAACGTATAGAAA-----GCTAATTAACAATCGTGGCG 4146  
 Db 688 TGACGTTTACATAGAATAACTCGTGTAAAGAAATCCTATAGGGGAGCTAAACAATCGTGGCG 747  
 QY 4147 TTTTCGGAATGACAGGAGAGGCCATACAGGAGCAAAAACAGCATGCTTTCTTAAACAGGTA 4206  
 Db 748 TTTTCGGAATGACAGGAGAGGCCATACAGGAGCAAAAACAGCATGCTTTCTTAAAGCAGGTG 807  
 QY 4207 ACACATGTCATCATTTCTTTTCATCAACATGTTGTCCATTTGCATTTACTGTACCTTCCA 4266  
 Db 808 CCATTTGTCATTTTATATATCGTCAAAATGTTTCTTATTGTAGTACTGTAGCTTCCA 867  
 QY 4267 CTGTTCTGTCACACTTCCAGCAGCTATACCTACGATATCTTCAATCTCTCCACTTAA 4326  
 Db 868 CTGTTCTTACTCCACACTTCCAGCAGCTATACCTACCTACGATACGAGATTTCTCCACA 927  
 QY 4327 CTTTCGSCACCATTAATAAATAAGAAATCTTTGCAAAATTTGTTTGAATATAGCATAGAT 4386  
 Db 928 TATTTCTCCACTTAGCTTCGGCACCATTAATACT--AAATATAGATAAATAATATCTTTT 986









CC encodes a floral meristem identity gene product (see AAW23812) that is  
 CC involved in the conversion of shoot meristem to floral meristem. Mutation  
 CC of the *API* gene results in replacement of a few basal flowers by  
 CC inflorescence shoots that are not subtended by flowers. When *API* is  
 CC ecotopically expressed in shoot meristem, the shoot meristem is converted  
 CC to floral meristem and early flowering can occur. The invention relates  
 CC to floral meristem identity genes *API*, *LFY* and especially *CAL* (see  
 CC AAT76885-97 and AAT99437) and their use in converting shoot meristem to  
 CC floral meristem and in promoting early flowering in transgenic plants,  
 CC especially angiosperms such as cereal plants, leguminous plants, oilseed  
 CC plants, trees, fruit-bearing plants or ornamental flowers  
 CC  
 CC  
 CC  
 CC Sequence 1860 BP; 610 A; 315 C; 339 G; 596 T; 0 U; 0 Other:  
 XX  
 SQ

Sequence 1860 BP; 610 A; 315 C; 339 G; 596 T; 0 U; 0 Other;

Query Match 8.8%; Score 470.4; DB 2; Length 1860;

Best Local Similarity 60.8%; Pred. No. 4e-70;

Matches 1213; Conservative 0; Mismatches 576; Indels 207; Gaps 19;

3423 GCACCTGAGTCCGACGTCAAATGATTTCAATAAATATTTCTCCTTTTAAATCCACATATAT 3482

[illegible]

I GCACCGAGTCCGACTCCGAATGTAACCAATTTCTCTCCATTAACCTATATATAAAATTAATAAT 60

3483 ATTATATCAATCTATTTGTAGTATTGATGAATTTTATTTGTATAAAACCTTCTGGTACACA 35

b  
61 ATTA TTT CAGT AAT AGTG ATATA TAT - - - - CTAT ATCT GTAT ATA AT CTCT CATATA 113

6T ATTATTCAGIATTAGIGATATATA-----CTTATCTGTAATAACTTGGAGATATA 11

3543 GACAACTGGTCGATGGAGTATAACAGGCTTAAGGCTTTGAGAGAGAAA 3602

b  
114 GAGGACCTCGTCGATCCGCCTATTATCCCTTATGCCCTATGGCTATCCTCACCTTTCCCCTCA

[illegible]

3603 CCAGAGGTACACATT--TACACTCATCACATTTCTATCTAGAAAATCGATCGGGTTCCAT 3604

174 CCAGAGGTACATTTTCATTCATCATTTATATAGATGAATATCAACAGGATTAAT 233

234 GTAGTTAAATGCATGATTACTTATAAGAAATGATGCATTATAACAAAAAATG 29

3680 CATTGATG--CTATTGAAATTCAGGCATTATCTTGGGAAGACTTGCAAGCAATGAGCCC 3737

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5' CATCGTCTCCTGTTATTAAGGCATTACTTCGGGAAGACTTCCATAGCATGAGCCC 333

3738 TAAAGAGCTTCAGAAATCTGGAGCAGCAGCTTGACACTGCTCTTAAGCACATCCGCACTAG 37

354 TAAGGAATCCAGAACTCTAGAGCAACAGCTTGATCTGCTCTTAAGCACATCCGCTCTAG 413

5' TTTGGGTTTCTTCCGAGTATCTAGAGGCAACAGGCTTGTATACCTGCTCTTAAAGCACAATCCGCTCTTAG 4'

3798 AAAAGTATGGCTTCGCTAATTCGTGAACTATCTATATAACTTAAACGTTTACAAGT 3857

414 AAAAGTATGAATCCCTCTATTCTTTAATTAAACATGTATCAACTTAAAC-----46

3858 GTTATTATAATGTGAACATTGAAATACATATGTGTATGTATCAATATATATATATCGTAAAT 3917

7  
3638 GTATATAAGTGGACCATGGAATACCAATAGTGTAAGTCAATATATATATCAGTAAAT 39

464 -----ACATATTTTATTATTCAATACATATATGAATAGTACATAT 508

3918 CAATATCAATTGATATGTCTATAGGTTGGTTCCGAATGTATGAGTTATGTTCTCTATTTT

50 9

509 GTGATTTTATTGGTTGGATATAAAAAGATCAATCACGTCGATTAGATGT-ATGACTTTT 560



Qy	4623	TATATAGTTCCTTCACCTTTGAAAATTTGATGANGATATAATGGTTTGAAATATAAATTTGCTG	4686
Db	1480	CAAACTGGTGTGCAAAATTTGAAACT-----TG	1506
Qy	4683	GCAGATCAAGGAGAGGGAATAATTTCTTAGGCTCAACAGAGCAGTGGATCAGCAGAA	4742
Db	1507	TCAGATTTAAGGAGAGGGAACAGTTCTTAGGGCGCAACAGAGCAATGGGACGAGCAGAA	1566
Qy	4743	CCAAAGGCCACAATATGGCTCCCTCCCTGCCCACCCAGCAGCACCACAAATCCAGCATCCTTA	4802
Db	1567	CCATGGCCATAATATGCTCGGCTCCACCCCGCAGCAGCATCAATCCAGCATCCTTA	1626
Qy	4803	CATGCTCTCTCATCAGCGCATCTCCTTTTCAACATGGGTAAACAAAAATTTACTAATCA	4862
Db	1627	CATGCTCTCTCATCAGCGCATCTCCTTTTCAACATGGGTAGTTAAAAAT---TCGTTTC	1683
Qy	4863	GTCTTAATTTAAAGCACATATGTTATGCA-AGCTAGTTTAGTTAGGTTGTTAATTTTCAT	4921
Db	1684	CTCTTACTTTCAAGTACATATGTTTATATACAAGATAGTTAGGTGTTATTAAGTCCAG	1743
Qy	4922	TGAAGTTATAGCTGTTAGTGATGGTTACATGATGCTAGATTTTGAAACTAGAAAACTTTA	4981
Db	1744	TGAGTTAAGTTGCTAGTGATGGTTAGTG--TCTAAATTTGCAATACAAGTACTAAG	1801
Qy	4982	TTTTAAACACATATTTTATTAAACGTA-----GGTTAATGCAATGGTCGCAACAGCAAA	5036
Db	1802	ATTTTCATGTATATATTTAAACGTAATTAATCATCAATCAAAATGGTCGTTAAAGAAACAG	1861
Qy	5037	ACTTATTAGTGTGAAAAATGTACATGGAATGGTTGCGAAAGCCTAAGTCGACTTTTG-	5095
Db	1862	ACTTATATTTTGGGAAAA-GTAGATGGAATGGCTGCTAAAGTCTAAGAAACCTTTGGG	1920
Qy	5096	---TTGTTGTGTCTATGTGTTTAAAGTCAAAATTTAGTTTGTGTAGATAAATGAAATTA	5152
Db	1921	AGCAGGTGCTTTTATTGTTGTTCAAATTAACCTTGAGGTAGTTAGTATAATAACTATC	1980
Qy	5153	TATATCTTTGACATTTCAAAATGCAATGATATTTGATTTTTCCTTTGTTGTGACGGTAAAC	5212
Db	1981	TTTGATATGGGCCCTTACCAATTTTCACTACAAAAA--TGTGATATTTTTCAGCACCTATGT	2039
Qy	5213	ATATGATTACATATGCACCTTTTCATATATATCCTATGTATGATGTTGATGATGCTGCTG	5272
Db	2040	AGATAATTTTGTAGCTATATCATGTGCA-----TATGAAATGTAATCTAGAGGGCTG	2092
Qy	5273	TATCAAGAAGATGATCCAATGGCAATGAGGAGAAATGATCTCGAACTGACTTTTGAACCC	5332
Db	2093	TATCAAGAAGATCAATGGCAATGAGGAGGACGATCTCGATCTGTCTCTTTGAACCC	2152
Qy	5333	GTTTACAACTGCAACCTTTGGCTG	5355
Db	2153	GTTTACAACTGCAACCTTTGGCCG	2175

## RESULT 10

AAC61417

ID AAC61417 standard; DNA; 2185 BP.

XX  
XX

AAC61417;

XX

DT 19-FEB-2001 (first entry)

XX

DE Genomic DNA sequence encoding an APETALA1 (AP1) polypeptide.

XX

KW APETALA1; AP1; floral meristem identity gene; CAULIFLOWER; CAL; LEAFY;

KW LFY; floral meristem; early flowering; ds.

XX

OS Brassica oleracea var. botrytis.

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100	100

PN US6127123-A.

	C
	C
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	C
	E
	G
	C
	C
	C
X	X
X	X
X	X

PD 03-OCT-2000.  
yy

PF	09-SEP-1998;	98US-00149976.		
XX				
PR	26-JAN-1996;	96US-00592214.		
XX				
PA	(REGC ) UNIV CALIFORNIA.			
XX				
PI	Yanofsky MF;			
XX				
DR	WPI; 2000-618379/59.			
XX				
PT	Identifying a Brassica having a cauliflower phenotype involves detecting a polymorphism associated with cauliflower locus comprising a modified cauliflower allele that does not encode active cauliflower gene product.			
PT				
XX				
PS	Disclosure; Fig 12A-C; 93pp; English.			
XX				
CC	The present sequence represents the genomic sequence of an APETALA1 (AP1) gene. The Api polypeptide is an ectopically expressible floral meristem identity gene product. The specification also describes cauliflower (CAL) and LEAFY (LFY) gene products. CAL is involved in the conversion of shoot meristem to floral meristem. CAL is highly conserved among different angiosperms. The CAL polynucleotides may be used to shoot meristem to floral meristem, and to promote early flowering in angiosperms			
XX				
SQ	Sequence 2185 BP; 719 A; 353 C; 409 G; 698 T; 0 U; 6 Other;			
Query Match 7.3%; Score 390.4; DB 3; Length 2185;				
Best Local Similarity 59.4%; Pred. No. 1.3e-56;				
Matches 1262; Conservative 0; Mismatches 494; Indels 367; Gaps 21;				
Qy	3300	TATTTATATATAATAATGATAATTGGTTGATGATA--AAGCTAACCCATAATCTGTGAAA 3357		
Db	353	TATGTATATATATGATCATATAAATTTGTTGATGATAAGAAGCTAGCCCTAATTTCTGTGAAT 412		
Qy	3358	TGATCAGTATGGAGAAGATCTTGAACGCTATGAGAGGTACTCTTACGCCGAAGACAGC 3417		
Db	413	TGAACAGTATGGAGGAGATCTTGAACGCTATGAGAGATCTCTTACGCCGAGAGACAGC 472		
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KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
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AC AA15016;
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XX API; promoter; transgenic plant; suppressed flowering; wood;
XX agamous-like protein; floral organ selective regulatory element; ss.
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DR P-PSDB; AAY84912.
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XX Transgenic plants in which flowering is suppressed by a tissue specific
XX cytotoxic gene product, useful for the production of wood for use as
XX lumber or pulp.
XX
XX Disclosure; Fig 8a-b; 79pp; English.
XX
XX The present sequence encodes the Arabidopsis API protein. The API
XX promoter is used to produce transgenic plants of the invention, which are
XX characterized by suppressed flowering. The plants are transformed with a
XX construct comprising a floral organ selective regulatory element (e.g.
XX API promoter), operatively linked to a nucleotide sequence encoding a
XX cytotoxic gene product (which is inheritable by the progeny). The plants
XX may be grown for either human consumption or for use as a raw material in
XX industry. When trees, they are particularly suitable for cultivation to
XX provide wood. As the flowering process consumes 20-35% of the energy of a
XX typical plant, it is advantageous to suppress flowering in order to
XX improve wood and lumber yields. Suppression of flowering may be desired
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XX dissemination
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XX QY 2015 CCACTGATTTCTTG 2027
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XX RESULT 15
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XX XX 18-JUN-1998 (first entry)
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XX CAULIFLOWER; CAL; LEAFY; LFY; reproductive development; angiosperm; ds.
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GenCore version 5.1.6  
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- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	5100.4	95.0	99698	8	AC008262	AC008262 Genomic s
2	4486.2	83.6	4708	8	AF466783	AF466783 Arabidops
3	4464.4	83.2	4710	8	AF466778	AF466778 Arabidops
4	4462.4	83.1	4711	8	AF466779	AF466779 Arabidops
5	4457	83.0	4710	8	AF466776	AF466776 Arabidops
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8	4449.2	82.9	4709	8	AF466773	AF466773 Arabidops
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16	4412.2	82.2	4706	8	AF466774	AF466774 Arabidops
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21	1790.4	33.4	1838	6	AX411721	AX411721 Sequence
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25	415.4	7.7	1786	8	AF126726	AF126726 Brassica
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36	310.2	5.8	1782	8	AF126730	AF126730 Brassica
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45	288.6	5.4	1787	8	AF126722	AF126722 Brassica

# ALIGNMENTS

RESULT 1  
AC008262/c  
LOCUS AC008262  
DEFINITION Genomic sequence for Arabidopsis thaliana BAC F4N2 from chromosome 1, complete sequence.  
ACCESSION AC008262  
VERSION AC008262.4 GI:5757471  
KEYWORDS HTG.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 99698)  
AUTHORS Shinn, P., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Khan, S., Kim, C.,

TITLE	Altafi, H., Araujo, R., Conn, L., Conway, A.B., Gonzalez, A., Hansen, N.F., Huizar, L., Kremenetskaia, I., Lenz, C., Li, J., Liu, S., Lueros, S., Rowley, D., Schwartz, J., Toriumi, M., Vysotskaia, V., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and Ecker, J.R.
	Genomic sequence for Arabidopsis thaliana BAC F4N2 from chromosome 1
JOURNAL	Unpublished
	2 (bases 1 to 99698)
REFERENCE	Ecker, J.R.
	Direct Submission
JOURNAL	Submitted (31-JUL-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
	3 (bases 1 to 99698)
REFERENCE	Ecker, J.R.
	Direct Submission
JOURNAL	Submitted (21-AUG-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
	4 (bases 1 to 99698)
REFERENCE	Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
	Direct Submission
JOURNAL	Submitted (22-JAN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
	5 (bases 1 to 99698)
REFERENCE	Chou, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
	Direct Submission
JOURNAL	Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
	6 (bases 1 to 99698)
REFERENCE	Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
	Direct Submission
JOURNAL	Submitted (11-OCT-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
	On Aug 21, 1999 this sequence version replaced gi:5733851. Location/Qualifiers
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F.T.A."

CDS	28229.	.28462
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CDS

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Query Match          95.0%; Score 5100.4; DB 8; Length 99698;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 5323; Conservative 0; Mismatches 31; Indels 24; Gaps 18.
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[illegible]

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DEFINITION Arabidopsis thaliana Ler apetala 1 (Api) gene, partial cds.  
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KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 4708)  
Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and  
Purugganan,M.D.

REFERENCE  
AUTHORS Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral  
Developmental Pathway  
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MEDLINE 21969421  
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Db	3891	ATATAGACATCTACTCTTAATTTATTAATAAATGTTTAAATAGTTCATTCATGAGTGAACCTG	3950
QY	4594	TGAAATTAATCTTTGTAACCATTCATATATATAGTTTCTTCACTTTGAAATTTGATGA	4653



Db CCAAAAGAAAGGTCTACTTTGTTACTTCACTGTTACAGCTGAGAACATTAATAATAAAGC 600  
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QY TAGAGAAATGTTAATAAAGAAATTAATAAATAGATATTTTGGTTGGTTTCAGATTTGTT 1361  
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QY TCGTAGATCTACAGGAAATCTCCGCGTCAATGCAAGCGAAGGTGACACTTCGGGAAG 1421  
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Db GACAGTGGTCCGTACAAATGTTACTTACCAATTTCTCTTCACGAGAGGTGATATCAAA 840  
QY TTGTTTATTTTTCATATTTTAAAGTCCGAGTTTATTAATAAATCATGGACCGACATTA 1541  
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QY GCAACGAGAAACAGCTTTAGCTTTTCCGTAACCACTCTTAAGAAACCACTGTGGTTTTT 1661  
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QY TCTTAATGTTTCATACCAAGTCTGAGCTCTTCTTATATCTCTCTTGTAGTTCTTAT 1781  
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QY TGGGGTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1841  
Db TGGGGTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1200  
QY AATGGAAGGGTAGGTTCAATTTGAAGAGTAGAGAACAGATCAATAGACAGTGAC 1901  
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QY ATTCTCGAAAAGAGAGCTGGTCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTGA 1961  
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QY TTCTTGGAATCTCAACTTAATCTTACTTTTAAAGAAAGCTCATGAGATCTCTGTTCTCTGTGA 2081  
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QY ATAGTATTTTCCCTTAAAGTTGACTTGTGTTTGAAGAAAGCTCATGAGATCTCTGTTCTCTGTGA 2141  
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Db AACACACTAATATACCATAGTAATTAACCTTGTATATATTGTGCAATATTTATCAGCATCA 1679  
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Db TATCTTCAAACTCAAGAGCATATAGAAAGGTGTATGTTTAACTTTTGAACCTAGGGTTTGG 1739  
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Db ATCCCTAACCTAATAATGAATTTCTTTGTTCTCCTCAATAGCCATGCTTTTGAATTTGGGA 1799  
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QY GAGTTCGAGTTTAAATGAAGTGTGCTTTTCTTTTTCATATAT-AGTTGCAACTTGGATTA 2555  
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QY TAATTAATAAATATATGCGGACGAGAAATTAATTAATAATAGATATAGATAAATGTCATCA 2615  
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QY AATTTGAGAAATTTTATTTAGAAAGATATTTAACTTACGAGTGTGTTTTCAGCTGTA 2675  
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QY AATTTGAACTAGTGTGTTCTTTGCTACTTTGACTTTAGAAATTAAGAACTGAAACAA 2855  
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QY AGATGTCAAACTGTAGTAGGAGTCTTTGACCTCTCGGGATCCATAAAAAGAACTAACTC 2915  
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QY CATCTTAAATCGGCTCTTACCGATGGTCAAACTTAGCTTCCAAACAGCAACAGCTGTTT 2338  
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Db GGTCTATGATTCATCTGTTTGTATTAATTAAGGATCATAGAGATCGGTACTTGTATTT 2578  
QY GTTATAGGAAATCTTGGTTTAAATTCGATAAAACCATCATTTAGATTTATCTTAAATGTCA 3274  
Db GTTATAGGAAATCTTGGTTTAAATTCGATAAAACCATCATTTAGATTTATCTTAAATGTCA 2638  
QY TGAATTTTGGTCACTCCCATATTTTATATAAATAAATGATAATTTGGTTGATGATA 3334  
Db TGAATTTTGGTCACTCCCATATTTTATATAAATAAATGATAATTTGGTTGATGATA 2698  
QY AAGCTAACCCCTAATTTCTGTGAATGATCAGTATGGAAGATCTTGAACCGTATGAGAG 3394  
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REFERENCE	1 (bases 1 to 4711)
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purugganan,M.D.
TITLE	Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral Developmental Pathway
JOURNAL	Genetics 160 (4), 1641-1650 (2002)
MEDLINE	21969421
PUBMED	11973317
REFERENCE	2 (bases 1 to 4711)
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purugganan,M.D.
TITLE	Direct Submission
JOURNAL	Submitted (09-JAN-2002) Genetics, North Carolina State University, Campus Box 7614, Raleigh, NC 27695-7614, USA
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Best Local Similarity	98.9%; Pred. No. 0;
Matches 4671; Conservative	0; Mismatches 27; Indels 23; Gaps 17;
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QY	701 GGATATTGACTGAAAATAAGGGGTTTTTTCACACTTTGAAGATCTCAAAAGAGAAAACAT 760
Db	61 GGATATTGACTGAAAATAAGGGGTTTTTTCACACTTTGAAGATCTCAAAAGAGAAAACAT 120
QY	761 TACAA CGGAATTCATTGTAAAAGACTGATTAGCAAAATGTAGCAAAAGGTTTTTATGTG 820
Db	121 TACAA CGGAATTCATTGTAAAAGACTGATTAGCAAAATGTAGCAAAAGGTTTTTATGTG 180
QY	821 GTTTATTTCATATATGATTGACATCAAAATGTATATATATATATGCTGTTTATTATTACAAT 880
Db	181 GTTTATTTCATATATGATTGACATCAAAATGTATATATATATGCTGTTTATTATTACAAT 240
QY	881 ATATATGGATATAACGTACAAACTAAATATGTTGATTGACGAAAAAAAATATATGTTG 940
Db	241 ATATATGGATATAACGTACAAACTAAATATGTTGATTGACGAAAAAAAATATGTTG 300
QY	941 TTTTGATTACCAATAGCACATATTCACATGATTTTGTCTCTGATCATCTACAACCTTAAT 1000
Db	301 TTTTGATTACCAATAGCACATATTCACATGATTTTGTCTCTGATCATCTACAACCTTAAT 360
QY	1001 AAGAACACACCAATTTGAAAAATCTTTCGACAAAATACATATTTTTCGGTTTGAATTTTG 1060
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Db	241	TATATGGATATACGTCGACAACTAAATATGTTGATTGACGAAAAAATAATATGATGT	300
Qy	942	TTGATTAAACAATAGACACATATTCAACTGATTTTTGTCTCTGATCATCTACAACTTAATA	1001
Db	301	TTGATTAAACAATAGACACATATTCAACTGATTTTTGTCTCTGATCATCTACAACTTAATA	360
Qy	1002	AGAACACACAACATTCGAAAAAATCTTTTGTGACAAATACTATTTTGGGTTTGAATTTTGA	1061
Db	361	AGAACACACAACATTCGAAAAAATCTTTTGTGACAAATACTATTTTGGGTTTGAATTTTGA	420
Qy	1062	ATACTTACAATTAATCTTCTCGATCTTCTCTCTTCTTCTTAAATCTCGGTGACAAATCG	1121
Db	421	ATACTTACAATTAATCTTCTCGATCTTCTCTCTTCTTCTTAAATCTCGGTGACAAATCG	480
Qy	1122	TCGACGCAATACATATACACAGTTGTCAAATGGTTCTCAGCTCTACCAAAAACATCTATTG	1181
Db	481	TCGACGCAATACATATACACAGTTGTCAAATGGTTCTCAGCTCTACCAAAAACATCTATTG	540
Qy	1182	CCAAAAAGAAAGGTCTATTGTGACTTCACTGTTACAGCTGAGAACATTAATATAAAGC	1241
Db	541	CCAAAAAGAAAGGTCTATTGTGACTTCACTGTTACAGCTGAGAACATTAATATAAAGC	600
Qy	1242	AAATTTTCATATAACAAAGGGTCTCACCTTTATTCCAAAGAAATAGTGTAATAATAGGTTAA	1301
Db	601	AAATTTTCATATAACAAAGGGTCTCACCTTTATTCCAAAGAAATAGTGTAATAATAGGTTAA	660
Qy	1302	TAGAGAAATGTTAATAAAGGAAATTAATAATAGATATTTTGGTTGGTTCAGATTTTGT	1361
Db	661	TAGAGAAATGTTAATAAAGGAAATTAATAATAGATATTTTGGTTGGTTCAGATTTTGT	720
Qy	1362	TCGTAGATCTACAGGAAATCTCCGCGTCAATGCAAAAGCGAAGGTGACACTTTGGGGAAG	1421
Db	721	TCGTAGATCTACAGGAAATCTCCGCGTCAATGCAAAAGCGAAGGTGACACTTTGGGGAAG	780
Qy	1422	GACCAGTGGTCCGTACAAATGTTACTTACCCTTCTCTCACGAGACGTCGATAATCAAA	1481
Db	781	GACCAGTGGTCCGTACAAATGTTACTTACCCTTCTCTCACGAGACGTCGATAATCAAA	840
Qy	1482	TTGTTTATTTTTCATATTTTAAAGTCCGAGTTTATTTAAATAATCATGACCCGACATTA	1541
Db	841	TTGTTTATTTTTCATATTTTAAAGTCCGAGTTTATTTAAATAATCATGACCCGACATTA	900
Qy	1542	GTACGAGATATACCAATGAGAAAGTCGACACGCAATCCTTAAGAAACCACTGTGTTT	1601
Db	901	GTACGAGATATACCAATGAGAAAGTCGACACGCAATCCTTAAGAAACCACTGTGTTT	960
Qy	1602	GCMAACAGAGAAACCACTTTAGCTTTTCCCTAAAACCACTCTTACCCAAATCTCTCCA	1661
Db	961	GCMAACAGAGAAACCACTTTAGCTTTTCCCTAAAACCACTCTTACCCAAATCTCTCCA	1020
Qy	1662	TAAATAAAGATCCCGAGACTCAAAACAAGTCTTTTATTAAGGAAAGAAAGAAACCTT	1721
Db	1021	TAAATAAAGATCCCGAGACTCAAAACAAGTCTTTTATTAAGGAAAGAAAGAAACCTT	1080
Qy	1722	TCCTAATTTGGTTTCATACAAAGCTGAGCTCTCTTTATATCTCTCTGTAGTTTCTTAT	1781
Db	1081	TCCTAATTTGGTTTCATACAAAGCTGAGCTCTCTTTATATCTCTCTGTAGTTTCTTAT	1140
Qy	1782	TCGGGGTCTTTGTTTGTGTTTGGTCTTTTATAGATTAAGAAAGTTCTTAAAAAGGATCAAA	1841
Db	1141	TCGGGGTCTTTGTTTGTGTTTGGTCTTTTATAGATTAAGAAAGTTCTTAAAAAGGATCAAA	1200
Qy	1842	AATGGGAAGGGTACGGTTCAATTGAGAGGATAGAGAACAGATCAATAGACAAAGTGAC	1901
Db	1201	AATGGGAAGGGTACGGTTCAATTGAGAGGATAGAGAACAGATCAATAGACAAAGTGAC	1260
Qy	1902	ATTCTCGAAAAAGAGCTGGTCTTTTGTGAAGAAAGCTCATGAGATCTCTGTCTGTGA	1961
Db	1261	ATTCTCGAAAAAGAGCTGGTCTTTTGTGAAGAAAGCTCATGAGATCTCTGTCTGTGA	1320
Qy	1962	TGCTGAAGTTGCTCTTGTGTTGCTTCTCCCATAAAGGGGAACCTTTTCGAATCTCCACTGA	2021



QY	3095	TGTACCTAATTGTAGCAAAATTAAAGAAACCGCAGTTAGTAACTCGAAGCTAAAGACATAG	3151
Db	2459	TGTACCTAATTGTAGCAAAATTAAAGAAACCGCAGTTAGTAACTCGAAGCTAAAGACATAG	2518
QY	3155	GGTCTATGATTCATCTGTTTGTATTATATAAGGTATCATAGAGATCGGTACTTGATTT	3214
Db	2519	GGTCTATGATTCATCTGTTTGTATTATATAAGGTATCATAGAGATCGGTACTTGATTT	2578
QY	3215	GTTATAGGAATCTTGGTTTAAATGTCATAAAACCATCATTAGATTTATCCTAAAATGTGA	3274
Db	2579	GTTATAGGAATCTTGGTTTAAATGTCATAAAACCATCATTAGATTTATCCTAAAATGTGA	2638
QY	3275	TGATATTTTGGTCACATCTCCAVATTAATTATATAATAAAATGATAATTGGTTGATGATA	3334
Db	2639	TGATATTTTGGTCACATCTCCAVATTAATTATATAATAAAATGATAATTGGTTGATGATA	2698
QY	3335	AAGCTAACCCCTAAATCTGTGAAATGATCAGTATGGAGAAGATCTTGAACGCTATGAGAG	3394
Db	2699	AAGCTAACCCCTAAATCTGTGAAATGATCAGTATGGAGAAGATCTTGAACGCTATGAGAG	2758
QY	3395	GTACTCTTACGCCGAAGACAGCTTAATTGCACCTGAGTCCGACGCTCAATGTATTTCAATA	3454
Db	2759	GTACTCTTACGCCGAAGACAGCTTAATTGCACCTGAGTCCGACGCTCAATGTATTTCAATA	2818
QY	3455	AATAATTTCTCTTTTAAATCCACATATATATATATCAATCTATTTGATGATTTGATGAAT	3514
Db	2819	AATAATTTCTCTTTTAAATCCACATATATATATATCAATCTATTTGATGATTTGATGAAT	2878
QY	3515	TTTTATTGTATAAAACTTCTGGTACACAGACAACCTGGTCGATGGAGTATAACAGGCTTA	3574
Db	2879	TTTTATTGTATAAAACTTCTGGTACACAGACAACCTGGTCGATGGAGTATAACAGGCTTA	2938
QY	3575	AGGCTAAGATTGAGCTTTTGGAGAGAAACACAGAGGTACATTTTACACTCATCACATTTTC	3634
Db	2939	AGGCTAAGATTGAGCTTTTGGAGAGAAACACAGAGGTACATTTTACACTCATCACATTTTC	2998
QY	3635	TATCTAGAAAATCGATCGGGTTCCATTTTAAAGTAAGTTAAAAATTCATTGATGCTATTGA	3694
Db	2999	TATCTAGAAAATCGATCGGGTTCCATTTTAAAGTAAGTTAAAAATTCATTGATGCTATTGA	3058
QY	3695	AATTCAGGCATTTATCTTGGGGAAGACATTGCAAGCAATGAGCCCTAAAGAGCTTCAGAATC	3754
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QY	3755	TGGAGCAGCAGCTTGACACTGCTTCTTAAGCACATCCGCACTAGAAAAGTATTCGCTTCCTG	3814
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QY	3815	CTATTTTCGTTGAAACATATCTATATAACTTAAACGGTTTACAAGTGTATTATATATGTAAC	3874
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QY	3875	ATTGAAATACATATGTATGTATCAATATATATATATATATATATATATATATATATATAT	3934
Db	3239	ATTGAAATACATATGTATGTATCAATATATATATATATATATATATATATATATATATAT	3298
QY	3935	GTCTATAGGTTGGTTCCAAATGTATGAGTTATGTTGTATTTTTAAGACCTCCATATTACATT	3994
Db	3299	GTCTATAGGTTGGTTCCAAATGTATGAGTTATGTTGTATTTTTAAGACT-CATATTACTTT	3357
QY	3995	AAAGTAAATGGGTTGTTAATGCTGTGTGTATGCAAGAACCAACTTATGTACAGAGTCC	4054
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QY	4055	ATCAATTCAGCTCCAAAAAAGGTATGTAAACCCCTATCAAAATGTATGTCTTATAGAGAA	4114
Db	3418	ATCAATTCAGCTCCAAAAAAGGTATGTAAACCCCTATCAAAATGTATGTCTTATAGAGAA	3477
QY	4115	ACGTATAGGAAAGCTAATTAAACAATCGTCCGTTTCGGAAATACACAGAGAGAGCCCATAC	4174
Db	3478	ACGTATAGGAAAGCTAATTAAACAATCGTCCGTTTCAGAAATGACAGAGAGAGCCCATAC	3537

QY	4175	AGGAGCAAAACAGCATGCTTTCTTAAACAGGTAAACACATGTTCATCATTTCTCTTTTCATCAA	4234
DB	3538	AGGAGCAAAACAGCATGCTTTCTTAAACAGGTAAACACATGTTCATCATTTCTCTTTTCATCAA	3597
QY	4235	CATGTTGTCATTCATTCATGTTTACCTTCCACTGTTCTGCCTCCACACTTCCAGCCAAAGC	4294
DB	3598	CATGTTGTCATTCATTCATGTTTACCTTCCACTGTTCTGCCTCCACACTTCCAGCCAAAGC	3657
QY	4295	TATACCTACGATATCTTTCATATCTCCACTTAACTTCGGCACCATTAATAAATAAATAAGAAA	4354
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QY	4355	ATCTTTGCAAAATTTGTTTGAATAAGCATAGATGTTGTTCTATTTGATTCATATAATCACCAG	4414
DB	3718	ATCTTTGCAAA--TTGTTTGAATAAGCATAGATGTTGTTCTATTTGATTCATATAATCACCAG	3776
QY	4415	CCTGTACGTAGATATGGTTTTCGCGTTTAGTTTTAAGG--TGTCCTCGGATTTGAAAAATAT	4473
DB	3777	CCTGTACGTAGATATGGTTTTCGCGTTTAGTTTTAAGGTTGTCTCTCGGATTTGAAAAATAT	3836
QY	4474	TTTGAAATTCITTTTGAAATGTTTGTGCCCATCATTCCTTACTTTAGTCTCATCTATGTATATG	4533
DB	3837	TTGAAA-----CTTTGAAATGTTGTGCCCATCATTC--TACTTTAGTCTCATCTATGTATATG	3891
QY	4534	AATATAGACACTACTCTCTAATAT--AAAAATTATATATAGTTTCATTCGATGAGTGCAACT	4592
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QY	4593	GTGAAAAATACATTTTGTAAACATTGCATATATATAGTTTCTTCACATTTTGAAAAATTCGATG	4652
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QY	4653	ATGATAATATGTTTGTAAAAATAAATTTGCTGGCAGATCAAGGAGAGGGAAAAATTTCTTTAG	4712
DB	4012	ATGATAATATGTTTGTAAAAATAAATTTGCTGGCAGATCAAGGAGAGGGAAAAATTTCTTTAG	4071
QY	4713	GGCTCAACAGAGCAGTGGGATCAGCAGAACCAAGGCCACAATATGCTCTCCCTCTGCC	4772
DB	4072	GGCTCAACAGAGCAGTGGGATCAGCAGAACCAAGGCCACAATATGCTCTCCCTCTGCC	4131
QY	4773	ACCGCAGCAGCACCANAATCCAGCATCTTTACATGCTCTCTCATCAGGCATCTCCTTTTCT	4832
DB	4132	ACCGCAGCAGCACCANAATCCAGCATCTTTACATGCTCTCTCATCAGGCATCTCCTTTTCT	4191
QY	4833	CAACATGGGGTAAACAAAAATTAATAATCAGTCTTAATTTAAAGCACATATGTTATGCAA	4892
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DB	4252	GCTAGTTACGTTAGGTGTTGTAAATTTTCATTTGAAGTTATAGCTGTTAGTGATGTTTACATG	4311
QY	4953	ATG--CTAGATTTTGAACCTAGAAAACTTTATTTTAAAAACATTTATTTTATTAACGTAGGTT	5011
DB	4312	ATGTCATGATTTTGAACCTAGAAAACTTTATTTTAAAAACATTTATTTTATTAACGTAGGTT	4371
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DB	4372	AATGCAATGTCGCCAAACGAAACAAACTTATTAGTGTGG--AAAAATGTCATGGAATGGTT	4430
QY	5072	GCAGAAAGCCTAAGTCGAC--TTTTGTGTTGTTGGTCTATGTTTAAAGTACAAATTTTAG	5130
DB	4431	GCAGAAAGCCTAAGTCGACTTTTTGTGTTGTTGGTCTATGTTTAAAGTACAAATTTTAG	4490
QY	5131	TTTGTGTAGATAAATGAAATTAATATATCTTTGACATTTTCACATGGAATGATATTGATT	5190
DB	4491	TTTGTGTAGATAAATGAAATTAATATATCTTTGACATTTTCACAAATGGACTGATATTGATT	4550
QY	5191	TTCTTTGTTGTTACGGTGAAACATATGATATGCACTTTTCATATATATATCTTATGTA	5250
DB	4551	TTCTTTGTTGTTACGGTGAAACATATGATATATGCACTTTTCATATATATATCTTATGTA	4610
QY	5251	TGATTTGTAATCAGTGGTCTGTATCAAGAAGATATCCAATGGCAATGAGAGGAATGCA	5310

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DEFINITION Arabidopsis thaliana Chi-1 apetal 1 (Apl) gene, partial cds.  
ACCESSION AF466773  
VERSION AF466773.1 GI:20799343  
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SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
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AUTHORS Olsen, K.M., Womack, A., Garrett, A.R., Suddith, J.I. and  
Purugganan, M.D.  
TITLE Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral  
Developmental Pathway  
JOURNAL Genetics 160 (4), 1641-1650 (2002)  
MEDLINE 21969421  
PUBMED 11973317  
REFERENCE 2 (bases 1 to 4712)  
AUTHORS Olsen, K.M., Womack, A., Garrett, A.R., Suddith, J.I. and  
Purugganan, M.D.  
TITLE Direct Submission  
JOURNAL Submitted (09-JAN-2002) Genetics, North Carolina State University,  
Campus Box 7614, Raleigh, NC 27695-7614, USA  
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DEFINITION Arabidopsis thaliana Kent 6048 apetal1 (AP1) gene, partial cds.

ACCESSION AP466777

VERSION AP466777.1 GI:20799351

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 4709)

AUTHORS Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purugganan,M.D.

TITLE Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral Developmental Pathway

JOURNAL Genetics 160 (4), 1641-1650 (2002)

MEDLINE 21969421

PUBMED 11973317

REFERENCE 2 (bases 1 to 4709)

AUTHORS Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purugganan,M.D.

TITLE Direct Submission

JOURNAL Submitted (09-JAN-2002) Genetics, North Carolina State University, Campus Box 7614, Raleigh, NC 27695-7614, USA

FEATURES

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ORIGIN		Query Match 82.8%; Score 4444.2; DB 8; Length 4711;	
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		Matches 4660; Conservative 0; Mismatches 38; Indels 23; Gaps 17;	
QY	643	AGGCTTATGCAATATATGCTTTAAGCAATGCCGAATCTG--TTTTTTTTTTTTTGTATT	700
DB	1	AGGCTTATGCAATATATGCTTTAAGCAATGCCGAATCTGTTT-----TTTTTTT	60
QY	701	GGATATTTGACTGAAATAAGGGGTTTTTTCACATTTGAAGATCTCAAAAGAGAAACTAT	760
DB	61	GGATATTTGACTGAAATAAGGGGTTTTTTCACATTTGAAGATCTCAAAAGAGAAACTAT	120
QY	761	TACACCGGAAATCATTTGTAAGAGATGATTAAAGCAATTTAGCAAGGTTTTTATGTG	820
DB	121	TACACCGGAAATCATTTGTAAGAGATGATTAAAGCAATTTAGCAAGGTTTTTATGTG	180
QY	821	GTATTATTCATTATATGATTGACATCAAAATTTGATATATATATATATATATATATAT	880
DB	181	GTATTATTCATTATATGATTGACATCAAAATTTGATATATATATATATATATATATAT	240
QY	881	ATATATGGATATAACGTAACAACTAAATATGTTTGAATGACGAAAAAATAATATATATG	940
DB	241	ATATATGGATATAACGTAACAACTAAATATGTTTGAATGACGAAAAAATAATATATATG	300
QY	941	TTTGATTAAACATAGCACATATTCACCTGATTTTGTCTGCTCATCTACCAACTTAAT	1000
DB	301	TTTGATTAAACATAGCACATATTCACCTGATTTTGTCTGCTCATCTACCAACTTAAT	360
QY	1001	AGAACAACACAACTTGAAGAAATCTTTGACAAATACTATTTTGGGTTTGAATTTTG	1060
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DB	421	AATPACTTACAAATTTCTTCTCGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	480
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Db 601 CAAATTTGATAAACAAGGGTCTCACCTTATTCCTAAAGATAGTGTAAATAGGGTA 660  
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JOURNAL	Developmental Pathway
MEDLINE	Genetics 160 (4), 1641-1650 (2002)
PUBMED	21969421
REFERENCE	11973317
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Puruganan,M.D.
TITLE	Direct Submission
JOURNAL	Submitted (09-JAN-2002) Genetics, North Carolina State University,
FEATURES	Campus Box 7614, Raleigh, NC 27695-7614, USA
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Query Match	82.7%; Score 4441.4; DB 8; Length 4709;
Best Local Similarity	98.8%; Pred. No. 0;
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Qy	1001 AAGAACACAC AAATTGAAAAATCTTTG CAAAAATCTATTTTTGGGTTTGAATTTTG 1060
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Qy	1061 AATACTTACA AATTATTCTTCGATCT TCCTCTCTTCTTAATCTCGGTACAAATCC 1120
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Qy <td>4414</td> <td>GCCTGTACGTAGATATGGTTTGTCCGTTAGTTTAAAG-TGTCTCCGGATTGAAATA</td> <td>4472</td>	4414	GCCTGTACGTAGATATGGTTTGTCCGTTAGTTTAAAG-TGTCTCCGGATTGAAATA	4472
Db <td>3775</td> <td>GTCGTAGTAGATATGGTTTGTCCGTTTAAAGTTTGTCTCCGGATTGAAATA</td> <td>3834</td>	3775	GTCGTAGTAGATATGGTTTGTCCGTTTAAAGTTTGTCTCCGGATTGAAATA	3834
Qy <td>4473</td> <td>TTTTGAAATCTTTTGAATGTTTGTCCCATCATCTTACTTTAGTCTCATATCTATGTATAT</td> <td>4532</td>	4473	TTTTGAAATCTTTTGAATGTTTGTCCCATCATCTTACTTTAGTCTCATATCTATGTATAT	4532
Db <td>3835</td> <td>TTTGGAAA---CTTTGAAATGTTTGTCCCATCATCTTACTTTAGTCTCATATCTATGTATAT</td> <td>3889</td>	3835	TTTGGAAA---CTTTGAAATGTTTGTCCCATCATCTTACTTTAGTCTCATATCTATGTATAT	3889
Qy <td>4533</td> <td>GAATATAGACACTACTCTCTTAATTAAT-AAAAATGTTATAATAGTTCAATTCGATGAGTGCAC</td> <td>4591</td>	4533	GAATATAGACACTACTCTCTTAATTAAT-AAAAATGTTATAATAGTTCAATTCGATGAGTGCAC	4591
Db <td>3890</td> <td>GAATATAGACACTACTCTTAATTAATTAATAAATGTTATAATAGTTCAATTCGATGAGTGCAC</td> <td>3949</td>	3890	GAATATAGACACTACTCTTAATTAATTAATAAATGTTATAATAGTTCAATTCGATGAGTGCAC	3949
Qy <td>4592</td> <td>TGTGAAATAAATCTTTTGTAAACATTCGATATATATAGTTTCTTCACTTTGAAATAATGAT</td> <td>4651</td>	4592	TGTGAAATAAATCTTTTGTAAACATTCGATATATATAGTTTCTTCACTTTGAAATAATGAT	4651
Db <td>3950</td> <td>TGTGAAATAAATCTTTTGTAAACATTCGATATATATAGTTTCTTCACTTTGAAATAATGAT</td> <td>4009</td>	3950	TGTGAAATAAATCTTTTGTAAACATTCGATATATATAGTTTCTTCACTTTGAAATAATGAT	4009
Qy <td>4652</td> <td>GATGATAAATGTTTGAATAAATTTGCTGGCAGATCAAGGAGAGGGAAAAATTCCTTA</td> <td>4711</td>	4652	GATGATAAATGTTTGAATAAATTTGCTGGCAGATCAAGGAGAGGGAAAAATTCCTTA	4711
Db <td>4010</td> <td>GATGATAAATGTTTGAATAAATTTGCTGGCAGATCAAGGAGAGGGAAAAATTCCTTA</td> <td>4069</td>	4010	GATGATAAATGTTTGAATAAATTTGCTGGCAGATCAAGGAGAGGGAAAAATTCCTTA	4069
Qy <td>4712</td> <td>GGGCTCAACAGGAGCAGTGGGATCAGCAACCAAGCCACAATATGTCCTCCCTCTGC</td> <td>4771</td>	4712	GGGCTCAACAGGAGCAGTGGGATCAGCAACCAAGCCACAATATGTCCTCCCTCTGC	4771
Db <td>4070</td> <td>GGGCTCAACAGGAGCAGTGGGATCAGCAACCAAGCCACAATATGTCCTCCCTCTGC</td> <td>4129</td>	4070	GGGCTCAACAGGAGCAGTGGGATCAGCAACCAAGCCACAATATGTCCTCCCTCTGC	4129
Qy <td>4772</td> <td>CACCGCAGCAGCAAAATCCAGCATCTTACATGCTCTCTCATCAGCCATCTCCTTTTC</td> <td>4831</td>	4772	CACCGCAGCAGCAAAATCCAGCATCTTACATGCTCTCTCATCAGCCATCTCCTTTTC	4831
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Db <td>4190</td> <td>TCAACATGGGTTTGAACAAAAATTAATCAATCAGTCTTAATTTAAAGCAATATGTTATGCA</td> <td>4249</td>	4190	TCAACATGGGTTTGAACAAAAATTAATCAATCAGTCTTAATTTAAAGCAATATGTTATGCA	4249
Qy <td>4892</td> <td>AGCTAGTTACGTTAGGTGTTGTAATTTTCATTTGAAGTTATAGTCTGTAGTGATGTTACAT</td> <td>4951</td>	4892	AGCTAGTTACGTTAGGTGTTGTAATTTTCATTTGAAGTTATAGTCTGTAGTGATGTTACAT	4951
Db <td>4250</td> <td>AGCTAGTTACGTTAGGTGTTGTAATTTTCATTTGAAGTTATAGTCTGTAGTGATGTTACAT</td> <td>4309</td>	4250	AGCTAGTTACGTTAGGTGTTGTAATTTTCATTTGAAGTTATAGTCTGTAGTGATGTTACAT	4309
Qy <td>4952</td> <td>GATG-CTAGATTTTGAACATAGAAACCTTTATTTTAAACATTAATTTTAAACGATAGGT</td> <td>5010</td>	4952	GATG-CTAGATTTTGAACATAGAAACCTTTATTTTAAACATTAATTTTAAACGATAGGT	5010
Db <td>4310</td> <td>GATGCTAGATTTTGAACATAGAAACCTTTATTTTAAACATTAATTTTAAACGATAGGT</td> <td>4369</td>	4310	GATGCTAGATTTTGAACATAGAAACCTTTATTTTAAACATTAATTTTAAACGATAGGT	4369
Qy <td>5011</td> <td>TAATGCAATGTCGCAACCAACAACTTAATAGTGTGGAATAATGTACATGGAATGGT</td> <td>5070</td>	5011	TAATGCAATGTCGCAACCAACAACTTAATAGTGTGGAATAATGTACATGGAATGGT	5070
Db <td>4370</td> <td>TAATGCAATGTCGCAACCAACAACTTAATAGTGTGGAATAATGTACATGGAATGGT</td> <td>4428</td>	4370	TAATGCAATGTCGCAACCAACAACTTAATAGTGTGGAATAATGTACATGGAATGGT	4428
Qy <td>5071</td> <td>TGCGAAAAAGCCTTAAGTCGAC-TTTTGTGTTGTTGTTGTTGTTTAAAGTACAAATTTTA</td> <td>5129</td>	5071	TGCGAAAAAGCCTTAAGTCGAC-TTTTGTGTTGTTGTTGTTGTTTAAAGTACAAATTTTA	5129
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Qy <td>5130</td> <td>GTTTGTGATGATAAATGAATTAATATCTTTGACATTTTCAAAATGCAATGATTTTGAAT</td> <td>5189</td>	5130	GTTTGTGATGATAAATGAATTAATATCTTTGACATTTTCAAAATGCAATGATTTTGAAT	5189
Db <td>4489</td> <td>GTTTGTGATGATAAATGAATTAATATCTTTGACATTTTCAAAATGCAATGATTTTGAAT</td> <td>4548</td>	4489	GTTTGTGATGATAAATGAATTAATATCTTTGACATTTTCAAAATGCAATGATTTTGAAT	4548
Qy <td>5190</td> <td>TTTTCTTTTGTGTCGCGTGAACATATGATTTACATATGCAATTTTCAATATATATATATAT</td> <td>5249</td>	5190	TTTTCTTTTGTGTCGCGTGAACATATGATTTACATATGCAATTTTCAATATATATATATAT	5249
Db <td>4549</td> <td>TTTTCTTTTGTGTCGCGTGAACATATGATTTACATATGCAATTTTCAATATATATATATAT</td> <td>4608</td>	4549	TTTTCTTTTGTGTCGCGTGAACATATGATTTACATATGCAATTTTCAATATATATATATAT	4608
Qy <td>5250</td> <td>ATGATTTGGAATGCAATGCTGCTGATCAGAAAGATGATCCTTCAATGAGGAGGAATG</td> <td>5309</td>	5250	ATGATTTGGAATGCAATGCTGCTGATCAGAAAGATGATCCTTCAATGAGGAGGAATG	5309
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Qy <td>5310</td> <td>ATCTCGAACTGACTCTTGAACCCCGTTTACAACTGCAACCTTT 5350</td> <td></td>	5310	ATCTCGAACTGACTCTTGAACCCCGTTTACAACTGCAACCTTT 5350	
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RESULT 12

AP466772

LOCUS

DEFINITION

ACCESSION

VERSION

AP466772

Arabidopsis thaliana Bu-2 apetal

1 (API) gene, partial cds.

AP466772.1

GI:20799341

4707 bp

DNA

linear

PLN 15-MAY-2002





Db	4668	TCTCGAAATGACTTCTGAACCCGGTTTACAACGTCAACCTT	4707
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AF466781			
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DEFINITION	Arabidopsis thaliana Bs-1 apetala 1 (AP1) gene, partial cds.		
ACCESSION	AF466781		
VERSION	AF466781.1	GI:20799359	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurooids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1 (bases 1 to 4705)		
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purgunan,M.D.		
TITLE	Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral Developmental Pathway		
JOURNAL	Genetics 160 (4), 1641-1650 (2002)		
MEDLINE	21969421		
PUBMED	11973317		
REFERENCE	2 (bases 1 to 4705)		
AUTHORS	Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and Purgunan,M.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JAN-2002) Genetics, North Carolina State University, Campus Box 7614, Raleigh, NC 27695-7614, USA		
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REFERENCE  
1 (bases 1 to 4706)  
Olsen, K.M., Womack, A., Garrett, A.R., Suddith, J.I. and  
Purugganan, M.D.  
Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral  
Developmental Pathway  
Genetics 160 (4), 1641-1650 (2002)  
21969421  
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REFERENCE  
2 (bases 1 to 4706)  
Olsen, K.M., Womack, A., Garrett, A.R., Suddith, J.I. and  
Purugganan, M.D.  
Direct Submission  
Submitted (09-JAN-2002) Genetics, North Carolina State University,  
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Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and  
Purugganan,M.D.  
Contrasting Evolutionary Forces in the Arabidopsis thaliana Floral  
Developmental Pathway  
Genetics 160 (4), 1641-1650 (2002)  
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Olsen,K.M., Womack,A., Garrett,A.R., Suddith,J.I. and  
Purugganan,M.D.  
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QY 3932 TATGCTATAGTGTGGTTTCCGAATGATGAGTGTATGTTGTTATTTTAAAGACTCCCATATTA 3991  
Db 3299 TATGCTATAGTGTGGTTTCCGAATGATGAGTGTATGTTGTTATTTTAAAGACT-CAATATA 3357  
QY 3992 CTTAAAGTAATGGTGTGTTTAAATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4051  
Db 3358 CTTAAAGTAATGGTGTGTTTAAATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3417  
QY 4052 TCCATCAATGAGCTCCAAAAAAGGTATGTAACACCCCTATCAAAATGATGTTCTTATAGA 4111  
Db 3418 TCCATCAATGAGCTCCAAAAAAGGTATGTAACACCCCTATCAAAATGATGTTCTTATAGA 3477  
QY 4112 GAAACGTATAGAAAGCTTAATTAACAATCGTCCGTTTCGAAATGACAGGAGAGGCCA 4171  
Db 3478 GAAACGTATAGAAAGCTTAATTAACAATCGTCCGTTTCGAAATGACAGGAGAGGCCA 3537  
QY 4172 TACAGGAGCAACAGCATGCTTTCTAAACAGGTAACACATGTCATCTTCTTTCAT 4231  
Db 3538 TACAGGAGCAACAGCATGCTTTCTAAACAGGTAACACATGTCATCTTCTTTCAT 3597  
QY 4232 CAACATGTTGTCATTTGCAATGTTTACCTTCCACTGTTCTGCTCCACACTTCCAGCCA 4291  
Db 3598 CAACATGTTGTCATTTGCAATGTTTACCTTCCACTGTTCTGCTCCACACTTCCAGCCA 3657  
QY 4292 AGCTATACCTAGATATCTTCATATCTCCACTTAACCTTCGGCACCATTAAATAAAATAG 4351  
Db 3658 AG-----ACCTACGATATCTTCATATCTCCACTTAACCTTCGGCACCATTGAATAAAATAG 3713  
QY 4352 AAAATCTTGCATAATTTGTTTGAATAGCATAGATGTTGTTCTATGTTGATGATTAATCAC 4411  
Db 3714 AAAATCTTGCATAATTTGTTTGAATAGCATAGATGTTGTTCTATGTTGATGATTAATCAC 3772  
QY 4412 CAGCCTCTAGCATATGTTTCTGCTGTTTAAAGT-TCGTCCTCGGATTGAAA 4470  
Db 3773 CAGCCTCTAGCATATGTTTCTGCTGTTTAAAGTTCGTTCTGCTCGGATTGAAA 3832  
QY 4471 TATTTTGAATCTTTTGAATGTTTGTCCCATCTTACTTAGCTCATATCTATGTTAT 4530  
Db 3833 TATTTGAAA-----CTTTGAAATGTTGTCCTGTCATTC-TACTTAGCTCATATCTATGTTAT 3887  
QY 4531 ATGAATATAGACACTACTCTTAATTAT-AAAATGTTTATATAGTTTCAATGCTAGTGCA 4589  
Db 3888 ATGAATATAGACACTACTCTTAATTATTAATAAAGTTTAAATAGTTTCAATGCTAGTGCA 3947  
QY 4590 ACTGTGAAAATAACTATTGTTGAAATGTTTGTCCCATCTTACTTAGCTCATATCTATGTTAT 4649  
Db 3948 ACTGTGAAAATAACTATTGTTGAAATGTTTGTCCCATCTTACTTAGCTCATATCTATGTTAT 4007  
QY 4650 ATGATGATAATATGTTTGAATAAATTTGTTGTCAGATCAAGGAGAGGGAATAAATCT 4709  
Db 4008 ATGATGATAATATGTTTGAATAAATTTGTTGTCAGATCAAGGAGAGGGAATAAATCT 4067  
QY 4710 TAGGGCTCAACAGGAGCAGTGGGATCAGCAGAACCAAGGCCACAAATATGCTTCCCTCT 4769  
Db 4068 TAGGGCTCAACAGGAGCAGTGGGATCAGCAGAACCAAGGCCACAAATATGCTTCCCTCT 4127  
QY 4770 GCCACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 4829  
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QY 4830 TCTCAACATGGGGTAACAAAAATTTACTAATCAGTCTTAATTTAAAGCACATATGTTATG 4889  
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QY 4890 CAAGCTAGTTACGTTAGTGTGTTAAATTCATTTGAAGTTATAGTGTGTTAGTGTGTTAG 4949  
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QY 5009 GTTAATGCAATGGTGGCCCAACGAAACAACTTTATTTAGTGTGAAAATGTAATGTAATG 5068  
Db 4368 GTTAATGCAATGGTGGCCCAACGAAACAACTTTATTTAGTGTG-AAAATGTAATGTAATG 4426  
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Db 4487 TAGTTGTTAGATAAATGAAATTAATATATCTTTTGACATTTTCAACATGCGACTGATTTTG 4546  
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QY 5248 GTATGATTTGGAATGCAATGCGTCTGTTATCAAGAAAGATGATCCAATGGCAATGAGAGGAA 5307  
Db 4607 GTATGATTTGGAATGCAATGCGTCTGTTATCAAGAAAGATGATCCAATGGCAATGAGAGGAA 4666  
QY 5308 TGATCTCGAACTGACTCTTGAACCGGTTTACAACTGCAACCTT 5350  
Db 4667 TGATCTCGAACTGACTCTTGAACCGGTTTACAACTGCAACCTT 4709

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